

2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

Fig. 1

722 ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA  
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA  
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 |Cadherin Cleavage| 872 GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT  
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG  
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC  
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022 TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC  
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG  
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 TTT AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT  
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG  
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx| 1292 GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC  
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322 AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA  
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC  
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC  
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

Fig. 1 (cont.)

1502  
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC  
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1562  
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA  
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622  
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT  
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1682  
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA  
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742  
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT  
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802  
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT  
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862  
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC  
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1922  
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG  
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982  
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA  
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042  
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC  
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102  
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT  
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2162  
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC  
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2222  
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG  
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2282  
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG

FIG. 1 (cont.)

cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

3182 3212  
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG  
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3302 3332  
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT  
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG  
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3542 3572 |XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX  
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATC  
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3662 xxxxxxxxxxxxxxxxxxxxxxxx| 3692  
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TA  
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala ty

3782 3812 |xxxxxxxxxxxxxxxxxxxxxx

CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GA

leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn gl

FIG. 1 (cont.)

arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxx Coiled-Coil 2 xxxxxxxxxxxxxx 3932 xxxxx|  
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992  
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 |xxxx PBM xxxx|  
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
met val his gly met thr ser ser ser ser val val STP

4082 4112  
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172  
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232  
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292  
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352  
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412  
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442 4472  
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502 4532  
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562 4592  
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622 4652  
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

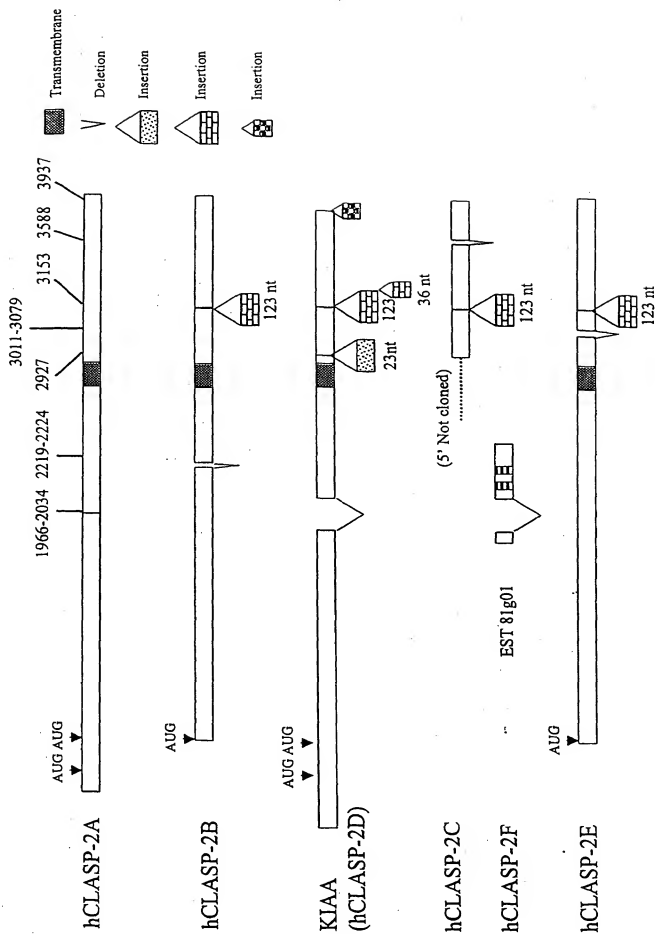
4682 4712  
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742 4772  
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802  
TTT ACT

Fig. 1 (cont.)

(Nucleotide position for insertions and deletion are found above the Human (h) CLASP-2A line diagram. Numbers are referenced based on hCLASP-2A nucleotide sequence from Figure 1.)



2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 2B



722 752  
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA  
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

762 812  
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA  
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 872  
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT  
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 932  
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG  
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 992  
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC  
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022 1052  
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC  
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 1112  
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG  
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 1172  
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT  
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 1232 ICadherin EC  
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG  
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx1 1292  
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC  
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322 1352  
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA  
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 1412  
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC  
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 1472  
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC  
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

Fig. 2B (cont.)

1502 1532  
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC  
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1562 1592  
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA  
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622 1652  
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT  
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1682 1712  
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA  
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742 1772  
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT  
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802 1832  
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT  
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862 1892  
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC  
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1922 1952 1xxxxxxxxxxxxxxxxxxxx  
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG  
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982 xxxxxxxxxx deleted in CLASP-2D(KIAA1058) xxxxxxxxxxxxxxxxxxxxxxxx  
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA  
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042 2072  
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC  
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102 2132  
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT  
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2162 2192 Deleted  
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC  
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

in HC2B  
xxx1 2252  
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG  
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

Fig. 2B (cont.)

2282 2312  
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG  
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372  
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT  
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432  
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC  
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492  
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT  
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552  
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC  
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612  
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC  
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672  
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC  
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732  
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG  
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792  
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG  
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 lxxxxxxxxxxxxxxx Predicted  
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC  
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

[Additional and differential exon usage found at position 2927 consisting  
of 69 nucleotides. This entire sequence is found in Human CLASP-2D  
(K1AA1058) and not other isoforms of CLASP-2. It has a sequence of:  
AAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCCCTGCGCTGAGGAGGCGGGGAG]

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA  
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972  
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA  
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu



3602 3632  
 AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA  
 ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662 3692  
 CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT  
 leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722 3752  
 GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG  
 ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782 3812  
 CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA  
 leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842 3872  
 CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA  
 arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

Insertion of 8 nucleotides found only in Human CLASP-2D with sequence: CTGGGATG

3902 3932  
 ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
 met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992  
 AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
 ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 1xxxx PEM xxxxi  
 ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
 met val his gly met thr ser ser ser val val STP

4082 4112  
 TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172  
 ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232  
 TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292  
 GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352  
 CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412  
 GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442 4472

CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502

4532

GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562

4592

TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622

4652

GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682

4712

TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742

4772

ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802

TTT ACT

Fig. 2B(cont.)

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058 GCATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGACAGCAAT  
 HC2E  
 HC2F

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058 AAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTTCGGAAACCTGAGAAGATG  
 HC2E  
 HC2F

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058 GCTAAGCTCCCAAGTGATTTTAGGCAATCTAGACATTACAATTGATAATGTTTCCTCAGAC  
 HC2E  
 HC2F

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058 TTCCCTAATTATGTTAATTATCATACATTCCCAACAAAACAAATTGAAACCTGCAGTAAA  
 HC2E  
 HC2F

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058 ACTCCCATCACGTTTGAAGTGGAGGAATTTGTGCCCTGCATACCAAAACACACTCAGCCT  
 HC2E  
 HC2F

FIG. 3A

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GAAGACTCTCAGCCCCTTAAGTGCAATTTATGGCAGACCTGGTGGGCCAGTTTTCACAAGA
HC2E	-----
HC2F	-----

HC2A	ATAGAGITGGCCCACTCAGCTGCATGAAAAAGCACCACTGTTGCTCACATTCTTCCATGTC
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATAGAGITGGCCCACTCAGCTGCATGAAAAAGCACCACTGTTGCTCACATTCTTCCATGTC
HC2E	-----
HC2F	-----



HC2A	GGCTACTCCTGGCTTCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GGCTACTCCTGGCTTCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2E	-----
HC2F	-----
HC2A	CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG
HC2E	-----
HC2F	-----
HC2A	CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2E	-----
HC2F	-----
HC2A	CATCTGGTTTCTACAGTGTATACTCAGGATCAGCATTTACATAAATTTTTCCAGTACTGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATCTGGTTTCTACAGTGTATACTCAGGATCAGCATTTACATAAATTTTTCCAGTACTGT
HC2E	-----
HC2F	-----
HC2A	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACTTGTAAGTACCTTAAGAGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACTTGTAAGTACCTTAAGAGT
HC2E	-----
HC2F	-----
HC2A	CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2-80	-----
HC2B	-----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2C	-----
HC2D-KIAA1058	CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2E	-----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2F	-----

Fig. 3A (cont.)

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

TTCCGAGTCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT  
 -----  
 TTCCGAGTCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT  
 -----  
 TTCCGAGTCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT  
 -----  
 TTCCGAGTCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT  
 -----  
 TTCCGAGTCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT  
 -----

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  
 -----  
 ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  
 -----  
 ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  
 -----  
 ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  
 -----  
 ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  
 -----

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA  
 -----  
 AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA  
 -----  
 AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA  
 -----  
 AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA  
 -----  
 AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA  
 -----

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  
 -----  
 CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  
 -----  
 CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  
 -----  
 CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  
 -----  
 CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  
 -----

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAAATCTATGGCTCAGCATTTG  
 -----  
 CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAAATCTATGGCTCAGCATTTG  
 -----  
 CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAAATCTATGGCTCAGCATTTG  
 -----  
 CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAAATCTATGGCTCAGCATTTG  
 -----  
 CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAAATCTATGGCTCAGCATTTG  
 -----

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACAGAGATTTCCTGCATCCTATCATCAT  
 -----  
 ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACAGAGATTTCCTGCATCCTATCATCAT  
 -----  
 ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACAGAGATTTCCTGCATCCTATCATCAT  
 -----  
 ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACAGAGATTTCCTGCATCCTATCATCAT  
 -----  
 ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACAGAGATTTCCTGCATCCTATCATCAT  
 -----

Flg. 3A (cont.)

HC2A GCAGCGGAAACCGTTGTAATAATGCTGATGCCACATCACTCAGAAGTTTGGAGATAAT  
 HC2-80 GCAGCGGAAACCGTTGTAATAATGCTGATGCCACATCACTCAGAAGTTTGGAGATAAT  
 HC2B GCAGCGGAAACCGTTGTAATAATGCTGATGCCACATCACTCAGAAGTTTGGAGATAAT  
 HC2C GCAGCGGAAACCGTTGTAATAATGCTGATGCCACATCACTCAGAAGTTTGGAGATAAT  
 HC2D-KIAA1058 GCAGCGGAAACCGTTGTAATAATGCTGATGCCACATCACTCAGAAGTTTGGAGATAAT  
 HC2E GCAGCGGAAACCGTTGTAATAATGCTGATGCCACATCACTCAGAAGTTTGGAGATAAT  
 HC2F GCAGCGGAAACCGTTGTAATAATGCTGATGCCACATCACTCAGAAGTTTGGAGATAAT

HC2A CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  
 HC2-80 CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  
 HC2B CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  
 HC2C CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  
 HC2D-KIAA1058 CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  
 HC2E CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  
 HC2F CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC

HC2A TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACATTAGCTGTTTTGCTCCT  
 HC2-80 TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACATTAGCTGTTTTGCTCCT  
 HC2B TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACATTAGCTGTTTTGCTCCT  
 HC2C TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACATTAGCTGTTTTGCTCCT  
 HC2D-KIAA1058 TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACATTAGCTGTTTTGCTCCT  
 HC2E TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACATTAGCTGTTTTGCTCCT  
 HC2F TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACATTAGCTGTTTTGCTCCT

HC2A GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  
 HC2-80 GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  
 HC2B GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  
 HC2C GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  
 HC2D-KIAA1058 GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  
 HC2E GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  
 HC2F GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT

HC2A GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  
 HC2-80 GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  
 HC2B GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  
 HC2C GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  
 HC2D-KIAA1058 GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  
 HC2E GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  
 HC2F GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC

HC2A CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACCTTCTTGGTG  
 HC2-80 CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACCTTCTTGGTG  
 HC2B CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACCTTCTTGGTG  
 HC2C CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACCTTCTTGGTG  
 HC2D-KIAA1058 CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACCTTCTTGGTG  
 HC2E CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACCTTCTTGGTG  
 HC2F CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACCTTCTTGGTG

HC2A	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCGGGGAGGTCCGCTCTGATC
HC2-80	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCGGGGAGGTCCGCTCTGATC
HC2B	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCGGGGAGGTCCGCTCTGATC
HC2C	-----
HC2D-KIAA1058	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCGGGGAGGTCCGCTCTGATC
HC2E	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCGGGGAGGTCCGCTCTGATC
HC2F	-----
HC2A	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2-80	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2B	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2C	-----
HC2D-KIAA1058	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2E	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2F	-----
HC2A	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2-80	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2B	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2C	-----
HC2D-KIAA1058	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2E	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2F	-----
HC2A	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2-80	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2B	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2C	-----
HC2D-KIAA1058	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACT
HC2E	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2F	-----
HC2A	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2-80	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2B	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2C	-----
HC2D-KIAA1058	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2E	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2F	-----
HC2A	AGCACCCCTGGACAAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2-80	AGCACCCCTGGACAAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2B	AGCACCCCTGGACAAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2C	-----
HC2D-KIAA1058	AGCACCCCTGGACAAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2E	AGCACCCCTGGACAAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2F	-----

Fig. 3A (cont.)

HC2A CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT  
 HC2-80 CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT  
 HC2B CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT  
 HC2C -----  
 HC2D-KIAA1058 CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT  
 HC2E CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTGAGAGGATCT  
 HC2F -----GCTGATTGAGAGGATCT

HC2A CTCATAAGCACAGATTGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC  
 HC2-80 CTCATAAGCACAGATTGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC  
 HC2B CTCATAAGCACAGATTGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC  
 HC2C -----  
 HC2D-KIAA1058 CTCATAAGCACAGATTGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC  
 HC2E CTCATAAGCACAGATTGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC  
 HC2F CTCATAAGCACAGATTGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC

HC2A CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCGGTGGTTCGCTGTGATAAACTT  
 HC2-80 CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCGGTGGTTCGCTGTGATAAACTT  
 HC2B CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCGGTGGTTCGCTGTGATAAACTT  
 HC2C -----  
 HC2D-KIAA1058 CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCGGTGGTTCGCTGTGATAAACTT  
 HC2E CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCGGTGGTTCGCTGTGATAAACTT  
 HC2F CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCGGTGGTTCGCTGTGATAAACTT

HC2A GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCTCTACATCTTAAAGAGCATGTCT  
 HC2-80 GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCTCTACATCTTAAAGAGCATGTCT  
 HC2B GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCTCTACATCTTAAAGAGCATGTCT  
 HC2C -----  
 HC2D-KIAA1058 GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCTCTACATCTTAAAGAGCATGTCT  
 HC2E GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCTCTACATCTTAAAGAGCATGTCT  
 HC2F GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCTCTACATCTTAAAGAGCATGTCT

HC2A GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT  
 HC2-80 GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT  
 HC2B GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT  
 HC2C -----  
 HC2D-KIAA1058 GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT  
 HC2E GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT  
 HC2F GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT

HC2A ACAAATATCTGAAGTCTGCCTGCACCAAGTTCAGTACATGGGGAAGCGATACATAGCCAGG  
 HC2-80 ACAAATATCTGAAGTCTGCCTGCACCAAGTTCAGTACATGGGGAAGCGATACATAGCCAGG  
 HC2B ACAAATATCTGAAGTCTGCCTGCACCAAGTTCAGTACATGGGGAAGCGATACATAGCCAGG  
 HC2C -----  
 HC2D-KIAA1058 ACAAATATCTGAAGTCTGCCTGCACCAAGTTCAGTACATGGGGAAGCGATACATAGCCAGG  
 HC2E ACAAATATCTGAAGTCTGCCTGCACCAAGTTCAGTACATGGGGAAGCGATACATAGCCAGG  
 HC2F ACAAATATCTGAAGTCTGCCTGCACCAAGTTCAGTACATGGGGAAGCGATACATAGCCAGG-

Fig. 3A (cont.)

HC2A AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC  
 HC2-80 AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC  
 HC2B AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC  
 HC2C -----  
 HC2D-KIAA1058 -----AA-----  
 HC2E AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC  
 HC2F -----TGTGA-----GAAAG-----ATATCAAGTGT-----

HC2A CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 HC2-80 CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 HC2B CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 HC2C -----  
 HC2D-KIAA1058 -----CAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 HC2E CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 HC2F -----GCTTGGAA-----

HC2A CTCACITTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 HC2-80 CTCACITTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 HC2B CTCACITTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 HC2C -----  
 HC2D-KIAA1058 CTCACITTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 HC2E CTCACITTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 HC2F -TTCTGTAGACAATGGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT

HC2A GAAGCCACACATTGCTACTGAGGTTTGCCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 HC2-80 GAAGCCACACATTGCTACTGAGGTTTGCCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 HC2B GAAGCCACACATTGCTACTGAGGTTTGCCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 HC2C -----  
 HC2D-KIAA1058 GAAGCCACACATTGCTACTGAGGTTTGCCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 HC2E GAAGCCACACATTGCTACTGAGGTTTGCCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 HC2F GAAGCCACACATTGCTACTGAGGTTTGCCCTGACAGCTCTGGACACGCTTTCTCTATTTACA

HC2A TTGGCGTTTAAAGAACACAGCTCCTGGCCGACCATTGGACATAATCCTCTCATGAAAAAAGTT  
 HC2-80 TTGGCGTTTAAAGAACACAGCTCCTGGCCGACCATTGGACATAATCCTCTCATGAAAAAAGTT  
 HC2B TTGGCGTTTAAAGAACACAGCTCCTGGCCGACCATTGGACATAATCCTCTCATGAAAAAAGTT  
 HC2C -----  
 HC2D-KIAA1058 TTGGCGTTTAAAGAACACAGCTCCTGGCCGACCATTGGACATAATCCTCTCATGAAAAAAGTT  
 HC2E TTGGCGTTTAAAGAACACAGCTCCTGGCCGACCATTGGACATAATCCTCTCATGAAAAAAGTT  
 HC2F TTGGCGTTTAAAGAACACAGCTCCTGGCCGACCATTGGACATAATCCTCTCATGAAAAAAGTT

HC2A TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGGCTTTAAAAAATGTC  
 HC2-80 TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGGCTTTAAAAAATGTC  
 HC2B TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGGCTTTAAAAAATGTC  
 HC2C -----  
 HC2D-KIAA1058 TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGGCTTTAAAAAATGTC  
 HC2E TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGGCTTTAAAAAATGTC  
 HC2F A-----

Flg. 3A (cont.)

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

TTCACCTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
TTCACCTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
TTCACCTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
-----  
TTCACCTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
TTCACCTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGTCTGTAACCCAAGCTGAGCTCC  
GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGTCTGTAACCCAAGCTGAGCTCC  
GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGTCTGTAACCCAAGCTGAGCTCC  
-----  
GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGTCTGTAACCCAAGCTGAGCTCC  
GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGTCTGTAACCCAAGCTGAGCTCC  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

ATCAGGACGGAGGCTCCAGCTGCTCTACTTCTCTGATGAGGAACAACCTTTGATTACACT  
ATCAGGACGGAGGCTCCAGCTGCTCTACTTCTCTGATGAGGAACAACCTTTGATTACACT  
ATCAGGACGGAGGCTCCAGCTGCTCTACTTCTCTGATGAGGAACAACCTTTGATTACACT  
-----  
ATCAGGACGGAGGCTCCAGCTGCTCTACTTCTCTGATGAGGAACAACCTTTGATTACACT  
ATCAGGACGGAGGCTCCAGCTGCTCTACTTCTCTGATGAGGAACAACCTTTGATTACACT  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

GGAAGAAGTCTCTTGTCCGGACACATTTGCAAGTCATCATATCTGTGACCCAGCTGATA  
GGAAGAAGTCTCTTGTCCGGACACATTTGCAAGTCATCATATCTGTGACCCAGCTGATA  
GGAAGAAGTCTCTTGTCCGGACACATTTGCAAGTCATCATATCTGTGACCCAGCTGATA  
-----  
GGAAGAAGTCTCTTGTCCGGACACATTTGCAAGTCATCATATCTGTGACCCAGCTGATA  
GGAAGAAGTCTCTTGTCCGGACACATTTGCAAGTCATCATATCTGTGACCCAGCTGATA  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

GCAGACGTGTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
GCAGACGTGTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
GCAGACGTGTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
-----  
GCAGACGTGTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
GCAGACGTGTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
-----  
TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
-----

Fig. 3A (cont.)

HC2A ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGCAC  
 HC2-80 ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGCAC  
 HC2B ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGCAC  
 HC2C  
 HC2D-KIAA1058 ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGCAC  
 HC2E ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGCAC  
 HC2F -----

HC2A CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCAGCGCCCGAG  
 HC2-80 CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCAGCGCCCGAG  
 HC2B CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCAGCGCCCGAG  
 HC2C  
 HC2D-KIAA1058 CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCAGCGCCCGAG  
 HC2E CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCAGCGCCCGAG  
 HC2F -----

HC2A CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA  
 HC2-80 CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA  
 HC2B CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA  
 HC2C  
 HC2D-KIAA1058 CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA  
 HC2E CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA  
 HC2F -----

HC2A GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA  
 HC2-80 GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA  
 HC2B GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA  
 HC2C  
 HC2D-KIAA1058 GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA  
 HC2E GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA  
 HC2F -----

HC2A G-----  
 HC2-80 G-----  
 HC2B G-----  
 HC2C  
 HC2D-KIAA1058 GAAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGG  
 HC2E G-----  
 HC2F -----

HC2A -----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAAACATC  
 HC2-80 -----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAAACATC  
 HC2B -----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAAACATC  
 HC2C -----GTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAAACATC  
 HC2D-KIAA1058 AGCGGGGGAGGGGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAAACATC  
 HC2E -----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAAACATC  
 HC2F -----

FIG. 3A (cont.)



HC2A GACGAGGAGGCCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCACGAGGAT  
 HC2-80 GACGAGGAGGCCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCACGAGGAT  
 HC2B GACGAGGAGGCCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCACGAGGAT  
 HC2C GACGAGGAGGCCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCACGAGGAT  
 HC2D-KIAA1058 GACGAGGAGGCCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCACGAGGAT  
 HC2E GACGAGGAGGCCCTCCATGATGGAAGACGTGGGGA-----  
 HC2F -----

HC2A GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG  
 HC2-80 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG  
 HC2B GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG  
 HC2C GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG  
 HC2D-KIAA1058 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG  
 HC2E GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG  
 HC2F -----AAGCCGAGCGCTACGAG-----

HC2A CTCATCGCGGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATT-----  
 HC2-80 CTCATCGCGGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATT-----  
 HC2B CTCATCGCGGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATTTTGAG  
 HC2C CTCATCGCGGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATTTTGAG  
 HC2D-KIAA1058 CTCATTGCGGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATTTTGAG  
 HC2E CTCATCGCGGACATCTACAAACTTATCATCCCCATTATGAGAAGCGGAGGGATTTTGAG  
 HC2F -----

HC2A -----  
 HC2-80 -----  
 HC2B AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCATG  
 HC2C AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCATG  
 HC2D-KIAA1058 AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCATG  
 HC2E AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCATG  
 HC2F -----

HC2A -----  
 HC2-80 -----  
 HC2B CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCGAGG-----  
 HC2C CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCGAGG-----  
 HC2D-KIAA1058 CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCGAGGCGAGG  
 HC2E CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCGAGG-----  
 HC2F -----

HC2A -----CTTTGAAGATGAAGATGGA  
 HC2-80 -----CTTTGAAGATGAAGATGGA  
 HC2B -----GATTCTTTGAAGATGAAGATGGA  
 HC2C -----GATTCTTTGAAGATGAAGATGGA  
 HC2D-KIAA1058 CAATACCAAGTTTACAGACAGTGAAACAGATGTGGAGGGATTCTTTGAAGATGAAGATGGA  
 HC2E -----GATTCTTTGAAGATGAAGATGGA  
 HC2F -----

Fig. 3A (cont.)

HC2A AAGGAGTATATTTACAAGGAACCCAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
 HC2-80 AAGGAGTATATTTACAAGGAACCCAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
 HC2B AAGGAGTATATTTACAAGGAACCCAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
 HC2C AAGGAGTATATTTACAAGGAACCCAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
 HC2D-KIAA1058 AAGGAGTATATTTACAAGGAACCCAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
 HC2E AAGGAGTATATTTACAAGGAACCCAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
 HC2F -----

HC2A CTTAAACTGTACTCGGATAAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC  
 HC2-80 CTTAAACTGTACTCGGATAAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC  
 HC2B CTTAAACTGTACTCGGATAAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC  
 HC2C CTTAAACTGTACTCGGATAAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC  
 HC2D-KIAA1058 CTTAAACTGTACTCGGATAAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC  
 HC2E CTTAAACTGTACTCGGATAAAATTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC  
 HC2F -----

HC2A AAGGTCAACCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
 HC2-80 AAGGTCAACCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
 HC2B AAGGTCAACCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
 HC2C AAGGTCAACCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
 HC2D-KIAA1058 AAGGTCAACCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
 HC2E AAGGTCAACCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
 HC2F -----

HC2A CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCAAC  
 HC2-80 CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCAAC  
 HC2B CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCAAC  
 HC2C CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCAAC  
 HC2D-KIAA1058 CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCAAC  
 HC2E CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCAAC  
 HC2F -----

HC2A ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
 HC2-80 ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
 HC2B ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
 HC2C ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
 HC2D-KIAA1058 ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
 HC2E ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
 HC2F -----

HC2A GAAGAGCAGTGCAAAACGGCGCACCATCTCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
 HC2-80 GAAGAGCAGTGCAAAACGGCGCACCATCTCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
 HC2B GAAGAGCAGTGCAAAACGGCGCACCATCTCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
 HC2C GAAGAGCAGTGCAAAACGGCGCACCATCTCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
 HC2D-KIAA1058 GAAGAGCAGTGCAAAACGGCGCACCATCTCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
 HC2E GAAGAGCAGTGCAAAACGGCGCACCATCTCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
 HC2F -----

HC2A AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  
 HC2-80 AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  
 HC2B AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  
 HC2C AAGCGCATCCCTTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGT--CCATT  
 HC2D-KIAA1058 AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  
 HC2E AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  
 HC2F -----

HC2A GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC  
 HC2-80 GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC  
 HC2B GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC  
 HC2C GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC  
 HC2D-KIAA1058 GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC  
 HC2E GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC  
 HC2F -----

HC2A ATGATCAAACGTCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTTCAGGTCAATGCTGGCCCA  
 HC2-80 ATGATCAAACGTCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTTCAGGTCAATGCTGGCCCA  
 HC2B ATGATCAAACGTCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTTCAGGTCAATGCTGGCCCA  
 HC2C ATGATCAAACGTCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTTCAGGTCAATGCTGGCCCA  
 HC2D-KIAA1058 ATGATCAAACGTCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTTCAGGTCAATGCTGGCCCA  
 HC2E ATGATCAAACGTCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTTCAGGTCAATGCTGGCCCA  
 HC2F -----

HC2A CTAGCATATGCGCGAGCTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA  
 HC2-80 CTAGCATATGCGCGAGCTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA  
 HC2B CTAGCATATGCGCGAGCTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA  
 HC2C CTAGCATATGCGCGAGCTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA  
 HC2D-KIAA1058 CTAGCATATGCGCGAGCTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA  
 HC2E CTAGCATATGCGCGAGCTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA  
 HC2F -----

HC2A GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG  
 HC2-80 GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG  
 HC2B GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG  
 HC2C GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG  
 HC2D-KIAA1058 GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG  
 HC2E GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG  
 HC2F -----

HC2A GTAAACGAACGCTCTGATTAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC  
 HC2-80 GTAAACGAACGCTCTGATTAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC  
 HC2B GTAAACGAACGCTCTGATTAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC  
 HC2C GTAAACGAACGCTCTGATTAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC  
 HC2D-KIAA1058 GTAAACGAACGCTCTGATTAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC  
 HC2E GTAAACGAACGCTCTGATTAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC  
 HC2F -----

FIG. 3A (cont.)

HC2A TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
 HC2-80 TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
 HC2B TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
 HC2C TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
 HC2D-KIAA1058 TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAGCTGGGATGATCTGCC  
 HC2E TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
 HC2F -----

HC2A CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCTTCACATCTTCAACGCCATCAGTG  
 HC2-80 CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCTTCACATCTTCAACGCCATCAGTG  
 HC2B CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCTTCACATCTTCAACGCCATCAGTG  
 HC2C CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCTTCACATCTTCAACGCCATCAGTG  
 HC2D-KIAA1058 CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCTTCACATCTTCAACGCCATCAGTG  
 HC2E CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCTTCACATCTTCAACGCCATCAGTG  
 HC2F -----

HC2A GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
 HC2-80 GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
 HC2B GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
 HC2C GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
 HC2D-KIAA1058 GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
 HC2E GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
 HC2F -----

HC2A ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCAATTTGCAAACCTCAGGATGCTTTCCAA  
 HC2-80 ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCAATTTGCAAACCTCAGGATGCTTTCCAA  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCAATTTGCAAACCTCAGGATGCTTTCCAA  
 HC2E -----  
 HC2F -----

HC2A AGCCAATCACTGGGGAGACCGAGCAACGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA  
 HC2-80 AGCCAATCACTGGGGAGACCGAGCAACGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 AGCCAATCACTGGGGAGACCGAGCAACGGGAGGACCA-GGGGAAGGGGAGAGAAAGGAAA  
 HC2E -----  
 HC2F -----

HC2A TAAAGAACAACGTTATTCTTAAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT  
 HC2-80 TAAAGAACAACGTTATTCTTAAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 TAAAGAACAACGTTATTCTTAAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT  
 HC2E -----  
 HC2F -----

HC2A TTTTAAATCTCACTGGCAATATTCAAAGTTTTCATTGTGTCTTAACAAAGGTGTGGTA  
 HC2-80 TTTTAAATCTCACTGGCAATATTCAAAGTTTTCATTGTGTCTTAACAAAGGTGTGGTA  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 TTTTAAATCTCACTGGCAATATTCAAAGTTTTCATTGTGTCTTAACAAAGGTGTGGTA  
 HC2E -----  
 HC2F -----

HC2A GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTAGAATAGATG  
 HC2-80 GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTAGAATAGATG  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTAGAATAGATG  
 HC2E -----  
 HC2F -----

HC2A GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT  
 HC2-80 GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT  
 HC2E -----  
 HC2F -----

HC2A GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGGAATCTGATCGTAATCAGGGTACAGAA  
 HC2-80 GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGGAATCTGATCGTAATCAGGGTACAGAA  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 GCCTGGGGGACCTTTTGCCTCGAGGCTGAGCTGGAATCTTGAAATATTTTTT---T  
 HC2E -----  
 HC2F -----

HC2A CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTGTGCTATTATCTCATTCA  
 HC2-80 CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTGTGCTATTATCTCATTCA  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 TTTCTGTGGCACATTGAGTTGAATACAAGAACTATTTTTGTGACTAGTTTTGTATGAC  
 HC2E -----  
 HC2F -----

HC2A ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG  
 HC2-80 ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 CTAAGGGAACCTGACCATTGTAATTTTGTACCAAGTGAACAGGAGATTAGTGCTTTTAT  
 HC2E -----  
 HC2F -----

Fig. 3A (cont.)

HC2A CTTCAAGTCAGAACITTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT  
 HC2-80 CTTCAAGTCAGAACITTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 ATTCATTTCTTGCAATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAACT  
 HC2E -----  
 HC2F -----

HC2A TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAAATTTGTG  
 HC2-80 TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAAATTTGTG  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCCGAACATATGCTGAAAAGTACA  
 HC2E -----  
 HC2F -----

HC2A CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTGATAAAAATGTGCAATAT  
 HC2-80 CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTGATAAAAATGTGCAATAT  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 AAGTAGTACAGTATATTGTTATGTACATATCATTTGTTAATACAGTCCTGGCATCTCTGTAC  
 HC2E -----  
 HC2F -----

HC2A GGAGATGTATACAAGTCITTTACT-----  
 HC2-80 GGAGATGTATACAAGTCITTTACT-----  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 ATATATGTATTACATTTCTACATTTTAACTACTCACATGGGCTTATGCATTAAGTTTAAT  
 HC2E -----  
 HC2F -----

HC2A -----  
 HC2-80 -----  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 TGTGATAAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTATTCTTGTACA  
 HC2E -----  
 HC2F -----

HC2A -----  
 HC2-80 -----  
 HC2B -----  
 HC2C -----  
 HC2D-KIAA1058 TAAAAATGTGCAATATGGAGATGTATACAGTCITTTACTATATTAGGTTTATAACAGTTT  
 HC2E -----  
 HC2F -----

Fig. 3A (cont.)

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

HC2A  
 HC2A-80  
 HC2B  
 HC2C  
 HC2D ASGNLDKNARFSATYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD  
 HC2E  
 HC2F

HC2A  
 HC2A-80  
 HC2B  
 HC2C  
 HC2D FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVPKYLYKYSQ  
 HC2E  
 HC2F

HC2A  
 HC2A-80  
 HC2B  
 HC2C  
 HC2D KSFARKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVTRSAFAAVLHHHQNPFEFYDEIK  
 HC2E  
 HC2F

HC2A  
 HC2A-80  
 HC2B  
 HC2C  
 HC2D IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLDGRVVTSEQHI  
 HC2E  
 HC2F

HC2A  
 HC2A-80  
 HC2B  
 HC2C  
 HC2D PVSANLPSGYLGQELGMGRHYGFEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC  
 HC2E  
 HC2F

HC2A  
 HC2A-80  
 HC2B  
 HC2C  
 HC2D OKTESGAQALGNELVKYLSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI  
 HC2E  
 HC2F



HC2A IHVVAQCHEEGLESHLRSYVKYAYKAEPPYVASEYKTVHEELTKSMTTILKPSADFLTSNK  
 HC2A-80  
 HC2B IHVVAQCHEEGLESHLRSYVKYAYKAEPPYVASEYKTVHEELTKSMTTILKPSADFLTSNK  
 HC2C  
 HC2D IHVVAQCHEEGLESHLRSYVKYAYKAEPPYVASEYKTVHEELTKSMTTILKPSADFLTSNK  
 HC2E IHVVAQCHEEGLESHLRSYVKYAYKAEPPYVASEYKTVHEELTKSMTTILKPSADFLTSNK  
 HC2F

HC2A LLRYSWFFFDVLIKSMQAHLIENSKVKLLRNQRFPSYHHAETVVNMLMPHITQKFGDN  
 HC2A-80  
 HC2B LLRYSWFFFDVLIKSMQAHLIENSKVKLLRNQRFPSYHHAETVVNMLMPHITQKFGDN  
 HC2C  
 HC2D LLKYSWFFFDVLIKSMQAHLIENSKVKLLRNQRFPSYHHAETVVNMLMPHITQKFRDN  
 HC2E LLRYSWFFFDVLIKSMQAHLIENSKVKLLRNQRFPSYHHAETVVNMLMPHITQKFGDN  
 HC2F

HC2A PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH  
 HC2A-80  
 HC2B PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH  
 HC2C  
 HC2D PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH  
 HC2E PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH  
 HC2F

HC2A EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI  
 HC2A-80  
 HC2B EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI  
 HC2C  
 HC2D EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI  
 HC2E EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTALQEFREVRLI  
 HC2F

HC2A AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRIINVRDVSPFPVNAGMT  
 HC2A-80  
 HC2B AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRIINVRDVSPFPVNAGMT  
 HC2C  
 HC2D AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRIINVRDVSPFPVNAGMT  
 HC2E AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRIINVRDVSPFPVNAGMT  
 HC2F

HC2A VKDESALPAVNPLVTPQKGSTLDNSLHKDLLGAI SGIASPYTTSTPNINSVRNADSRGS  
 HC2A-80  
 HC2B VKDESALPAVNPLVTPQKGSTLDNSLHKDLLGAI SGIASPYTTSTPNINSVRNADSRGS  
 HC2C  
 HC2D VKDESALPAVNPLVTPQKGSTLDNSLHKDLLGAI SGIASPYTTSTPNINSVRNADSRGS  
 HC2E VKDESALPAVNPLVTPQKGSTLDNSLHKDLLGAI SGIASPYTTSTPNINSVRNADSRGS  
 HC2F ADSRGS

HC2A LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNVVRCDKLDQSEIKSLLMCFLYILKSMS  
 HC2A-80 LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNVVRCDKLDQSEIKSLLMCFLYILKSMS  
 HC2B LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNVVRCDKLDQSEIKSLLMCFLYILKSMS  
 HC2C -----  
 HC2D LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNVVRCDKLDQSEIKSLLMCFLYILKSMS  
 HC2E LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNVVRCDKLDQSEIKSLLMCFLYILKSMS  
 HC2F LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNVVRCDKLDQSEIKSLLMCFLYILKSMS

HC2A DDALFTYWNKASTSELMDFFTISEVCLHQFYQMGKRYIARNQEGGLPIVHDRKSQTLPV  
 HC2A-80 DDALFTYWNKASTSELMDFFTISEVCLHQFYQMGKRYIARNQEGGLPIVHDRKSQTLPV  
 HC2B DDALFTYWNKASTSELMDFFTISEVCLHQFYQMGKRYIARNQEGGLPIVHDRKSQTLPV  
 HC2C -----  
 HC2D DDALFTYWNKASTSELMDFFTISEVCLHQFYQMGKRYIAR-----  
 HC2E DDALFTYWNKASTSELMDFFTISEVCLHQFYQMGKRYIARNQEGGLPIVHDRKSQTLPV  
 HC2F DDALFTYWNKASTSELMDFFTISEVCLHQFYQMGKRYIAS-----VR--KISSVLGIS

HC2A RNRRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT  
 HC2A-80 RNRRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT  
 HC2B RNRRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT  
 HC2C -----  
 HC2D ---TGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT  
 HC2E RNRRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT  
 HC2F V-----D-NG-----YGHSDADVLHQSLLEANIATEVCLTALDTLSLFT

HC2A LAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFEYGRA  
 HC2A-80 LAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFEYGRA  
 HC2B LAFK--LLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFEYGRA  
 HC2C -----  
 HC2D LAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFEYGRA  
 HC2E LAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFEYGRA  
 HC2F LAFKNQLLADHGHNPIMKK-----

HC2A DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQLI  
 HC2A-80 DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQLI  
 HC2B DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQLI  
 HC2C -----  
 HC2D DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQLI  
 HC2E DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQLI  
 HC2F -----

HC2A ADVVGIGETRFQQSLSIINNCCANS DRLIKHTSFSSDVKD LTKRIRTVLMATAQMKEHEND  
 HC2A-80 ADVVGIGETRFQQSLSIINNCCANS DRLIKHTSFSSDVKD LTKRIRTVLMATAQMKEHEND  
 HC2B ADVVGIGETRFQQSLSIINNCCANS DRLIKHTSFSSDVKD LTKRIRTVLMATAQMKEHEND  
 HC2C -----  
 HC2D ADVVGIGETRFQQSLSIINNCCANS DRLIKHTSFSSDVKD LTKRIRTVLMATAQMKEHEND  
 HC2E ADVVGIGETRFQQSLSIINNCCANS DRLIKHTSFSSDVKD LTKRIRTVLMATAQMKEHEND  
 HC2F -----

Flg. 3B (cont.)

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
HC2E  
HC2F

PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNKGLDSEAAMCYVHV TALVAEYLTRK  
PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNKGLDSEAAMCYVHV TALVAEYLTRK  
PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNKGLDSEAAMCYVHV TALVAEYLTRK  
PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNKGLDSEAAMCYVHV TALVAEYLTRK  
PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNKGLDSEAAMCYVHV TALVAEYLTRK  
PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNKGLDSEAAMCYVHV TALVAEYLTRK

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
HC2E  
HC2F

-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE  
-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE  
-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE  
-----FRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE  
EAVQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE  
-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
HC2E  
HC2F

DVLMELLEQCADGLWKAERYELIADIYKLIIP IYEKRR-----  
DVLMELLEQCADGLWKAERYELIADIYKLIIP IYEKRR-----  
DVLMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHYDTLHRAYSK  
DVLMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHYDTLHRAYSK  
DVLMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHYDTLHRAYSK  
DVLMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHYDTLHRAYSK  
-----KAERYELIADIYKLIIP IYEKRRD FERLAHYDTLHRAYSK

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
HC2E  
HC2F

-----DFFEDEDGKEYIYKEPKLTP LSE  
-----DFFEDEDGKEYIYKEPKLTP LSE  
VTEVMHSGRRLLGTYFRVAFPGQ-----GFFEDEDGKEYIYKEPKLTP LSE  
VTEVMHSGRRLLGTYFRVAFPGQ-----GFFEDEDGKEYIYKEPKLTP LSE  
VTEVMHSGRRLLGTYFRVAFPGQAQYQFTDSETDVEGFFEDEDGKEYIYKEPKLTP LSE  
VTEVMHSGRRLLGTYFRVAFPGQ-----GFFEDEDGKEYIYKEPKLTP LSE

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
HC2E  
HC2F

ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF  
ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF  
ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF  
ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF  
ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF  
ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF  
ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF

HC2A  
HC2A-80  
HC2B  
HC2C  
HC2D  
HC2E  
HC2F

ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRI PVMYQHHTDLNP  
ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRI PVMYQHHTDLNP  
ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRI PVMYQHHTDLNP  
ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRI PVMYQHHTDLNP  
ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRI PVMYQHHTDLNP  
ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRI PVMYQHHTDLNP  
ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRI PVMYQHHTDLNP

Fig. 3B (cont.)

HC2A	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGSSVSVQVNAGPLAYARAFLDDTNTKR
HC2A-80	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGSSVSVQVNAGPLAYARAFLDDTNTKR
HC2B	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGSSVSVQVNAGPLAYARAFLDDTNTKR
HC2C	IEVHZ-----
HC2D	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGSSVSVQVNAGPLAYARAFLDDTNTKR
HC2E	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGSSVSVQVNAGPLAYARAFLDDTNTKR
HC2F	-----

HC2A	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2A-80	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2B	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2C	-----
HC2D	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2E	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2F	-----

HC2A	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSVVZ----
HC2A-80	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSVVZ----
HC2B	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSVVZ----
HC2C	-----
HC2D	LG-----
HC2E	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSVVZ----
HC2F	-----

FIG. 3B(cont.)

PBL  
lung  
placenta  
sm intestine  
liver  
kidney  
spleen  
thymus  
colon  
skel muscle  
heart  
brain

FIG. 4A

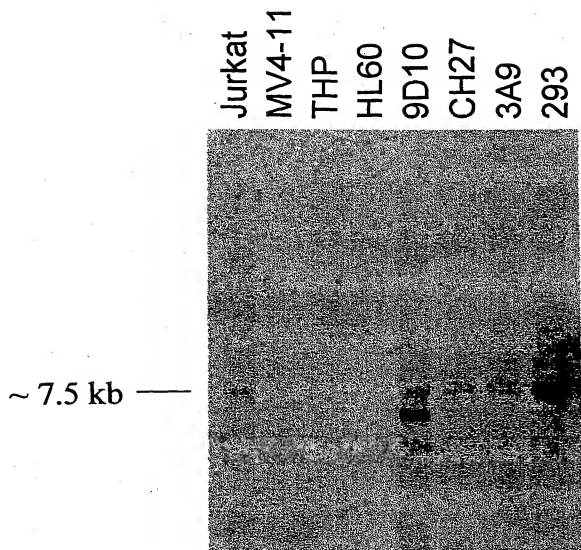


Fig. 4B

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

ASGNLDKNAFSAIYRQDSNKLSDNDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD  
-----  
-----  
-----  
-----  
-----  
-----

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ  
-----  
-----  
-----  
-----  
-----  
-----

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

-----VLHHHQNPEFYDEIK  
KSFARKARNIAICIEFKDSDEEDSQPLKCIYGRPGGFVTRSAFAAVLHHHQNPEFYDEIK  
-----  
-----  
-----  
-----  
-----

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRRVVTSEQHI  
IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRRVVTSEQHI  
-----  
-----  
-----  
-----  
-----

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

PVSANLPSGYLGYQELGMRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYIC  
PVSANLPSGYLGYQELGMRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYIC  
-----  
-----  
-----  
-----  
-----GPGPARSTVSIISLINSARV  
-----

HC2A  
KIAA  
rat  
HC4  
HC1  
HC3  
HC5

QKTESGAQALGNELVKYKLSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV  
QKTESGAQALGNELVKYKLSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV  
-----  
-----MEIQVLIRFLSVILNQLFWVLFNMIHEDDVPISCPMV  
-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV  
NRSRLSNSNPDISGTPSPDDEVRS IIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES  
-----

HC2A I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P V V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N  
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P V V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N  
 rat  
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P O A P L I H E T L A T M I A L L K Q S A D F L A I N  
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K  
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G --- S V R --- E  
 HC5

Cadherin  
 Cleavage

HC2A K L L R Y S W F F D V L I K S M A Q H L I E N S K V K L L R N Q R F P A S Y H H A E T V V N M L M P H I T Q K F G D  
 KIAA K L L K Y S W F F D V L I K S M A Q H L I E N S K V K L L R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D  
 rat  
 HC4 K L L K Y S W F F E I I A K S M A T Y L L E E N K I K L T H G O R F P K A Y H H A L H S L F L A I T - I V E S O Y A E  
 HC1 H V L K S W F F F A I I L K S M A Q H L I D T N K I Q L P R P O R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D  
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P K R S F P F E R M D D I A L V S T I A S I D V S R F O K  
 HC5

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L  
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L  
 rat  
 HC4 I P K E S R N V N Y S L A S F L K C C L T I M D R G F V F N L I N --- D Y I S --- G F S P K D P K V L A E Y K F E F L  
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V K M V N --- N Y I S --- M F S S G D L K T L C Q Y K F D E L  
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y Q V S S K L Y S L P N P S V L V S L R L D F L  
 HC5

HC2A R V V C N H E H Y I P L N L F M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F  
 KIAA R V V C N H E H Y I P L N L F M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F  
 rat  
 HC4 Q T I C N H E H Y I P L N L F M --- A F A K P K L Q R --- V Q D S N L --- E Y S L S D E Y  
 HC1 Q E V C Q H E H F I P I C L P I R S A N I P D L P T P S E S --- T Q E L H A S D M P E Y S V T N E F  
 HC3 R I I C S H E H Y V T I N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D K I A N M F E L S --- V P F  
 HC5 --- M N A D T A P T S P C P S I S --- S Q N S S C S S F Q D Q K I A S M F D R T S R V P A

HC2A C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H O A R I A T  
 KIAA C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H O A R I A T  
 rat  
 HC4 C K H H F L V G L L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q O A K I A Q  
 HC1 C R K V L F I G L I L R E V G F A L Q E D O D --- V R H L A L A V L K N I A M A K H S F D D R Y R E P R K Q A I A S  
 HC3 R Q Q H Y L A G L V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M  
 HC5 S T S - S P G L L F T L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H  
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H  
 rat  
 HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A M P N S A S R D E F F C G --- F T S P - A N - R G S L S  
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D L S T N G G F O S Q T A I K H A N S V D T S F S  
 HC3 L Y L P L I G I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M I S  
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- G A I T

HC2A K D L L G A I S G I A S P Y T T S T P N I N S V R N A D S R G S L I S T D S G N S L P E R N E S K N S L D K H Q Q S S  
 KIAA K D L L G A I S G I A S P Y T T S T P N I N S V R N A D S R G S L I S T D S G N S L P E R N E S K N S L D K H Q Q S S  
 rat  
 HC4 T K D T A Y G S F Q N G --- H G I K R E D S R G S L I P - E G A T G F P D Q G N T G E N --- T R Q S  
 HC1 C R K V L N S I A A F S S --- I A I S T V N H A D S R A S L A S L D N P S T N E K S S E K T D N C E K I P R P L  
 HC3 Q T V A M A I A G T S V F Q --- L T R P G S F L L T S T S G R O H T ---  
 HC5 Q N V A L A I A G N F N --- L K T S G - I V L S S L P Y K Q Y N ---



HC2A TLGNSVVRCDKLDQSEIKSLIMCFLYLKSMSSDALLFTYWN-KASTSELMDFFTISEVCL  
 KIAA TLGNSVVRCDKLDQSEIKSLIMCFLYLKSMSSDALLFTYWN-KASTSELMDFFTISEVCL  
 rat -----  
 HC4 STRSSVSQYNRLDQYEIRSLIMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL  
 HC1 ALIGSTLRFDRDLQAEIRSLIMCFLHIMKTISETLYLAYWQ-RAPSPVSDFFSILDVCL  
 HC3 -----TFSAESSRSLILCLLWLVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYCLV  
 HC5 -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFOYMGKRYIARNQEGLG--PIVHDRKS-----QTLPSVRNRTGMM  
 KIAA HQFOYMGKRYIAR-----TGMM  
 rat -----  
 HC4 FHFYMGKRNRIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM  
 HC1 QNFRYLGRKNIIRKIAAAF--KFVQSTQNNGTLKGSNPSQTSGLLAQWMHSTSRHEGKH  
 HC3 SCFEYKGGKVFERNLSLTFK--KSKDMRAK-----LEEAILGSI GARQEMV  
 HC5 LCFEYKGGKSSDKVSTQVLQ--KSRDVKAR-----LEEAIRGEGARGEMM

HC2A HARLQOL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC  
 KIAA HARLQOL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC  
 rat -----  
 HC4 QARLQHL-----SSLESS-----FTLNHSSSTTTEADIFHQALLEGNATEVS  
 HC1 QHRSQTLPIIRGK--NALSNNPKL--LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC  
 HC3 RRSRGQLERSPSGSAFGSQENLRWKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN  
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEAELISGNLATEAH

HC2A LTLADTLSLFTLAFKNQLLADHGHNPIMKKVFDVYLCLFQKHQSEETALKNVFTALRSLIY  
 KIAA LTLADTLSLFTLAFKNQLLADHGHNPIMKKVFDVYLCLFQKHQSEETALKNVFTALRSLIY  
 rat -----KLSRGHSPIMKKVFDVYLCLFQKHQSEETALKNVFTALRSLIY  
 HC4 LTVLDTISFFTQCFTHFLNNDGHNPIMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFTS  
 HC1 LTLILDVLSLFTQTHORLQOCCDQNSLMKRGFDTYMLFFOVNQSATALKHVFASLRLFVC  
 HC3 LTIILDTIEIVQTVS--VTES--KESILGGVLKVLHSHMACNQSAVYLQHCFCFATORHMLVS  
 HC5 LTIILMQENIIQASS--ALDC--KDSILGGVLRLVNSLNCQDSTTYLTHCFATLALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH  
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH  
 rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH  
 HC4 KFPFAFFQGRVNMCAAFCEYVLKCCSTKISSIRTEASALLYLMRNNFEYTKRKTFLRTH  
 HC1 KFPFAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLMRKNFEYFNKQKSIVRSK  
 HC3 KFPPELLFEEETEQQCADLCLRLLRHCSSSIGTIRSHPSASLYLIMRQNFIEIGN--NFAVRK  
 HC5 KFGDLLFEEVEEQCFDLCHQVLHHCSSSMVDTRSQACATLYLLMRFSFGATS--NFAVRK

HC2A LQVIISVSQLIADVVIGIGETRFOQSLSIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM  
 KIAA LQVIISVSQLIADVVIGIGETRFOQSLSIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM  
 rat LQVIISVSQLIADVVIGIGETRFOQSLSIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM  
 HC4 LQIIIVSVQLIADVALSGGSRFQESLFIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM  
 HC1 LQIIIVSVQLIADVALSGGSRFQESLFIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM  
 HC3 LQIIIVSVQLIADVALSGGSRFQESLFIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM  
 HC5 LQIIIVSVQLIADVALSGGSRFQESLFIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM

HC2A   ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKRTWLDSMARIHVKNGDLS~~EAAMCYVHV~~  
 KIAA   ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKRTWLDSMARIHVKNGDLS~~EAAMCYVHV~~  
 rat    ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKRTWLDSMARIHVKNGDLS~~EAAMCYVHV~~  
 HC4   ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKRTWLDSMARIHVKNGDLS~~EAAMCYVHV~~  
 HC1   ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKRTWLDSMARIHVKNGDLS~~EAAMCYVHV~~  
 HC3   ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKRTWLDSMARIHVKNGDLS~~EAAMCYVHV~~  
 HC5   DTVKMREHNDPEMLVDLQYSLAKSYASTPELRKRTWLDSMARIHVKNGDLS~~EAAMCYVHV~~

## SH3

HC2A   TALVAEYITRKGV-----VQWEPPLPHSHSACLRRSGGVFRQGCTAFRVITPN  
 KIAA   TALVAEYITRKEA-----VQWEPPLPHSHSACLRRSGGVFRQGCTAFRVITPN  
 rat    TALVAEYITRKEAD-----LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN  
 HC4   AALVAEYITRKKL-----FPNGCSAFTKPTPN  
 HC1   AALIAEYITRKGYWKVEKITASLLSEDTHPDCDSNLLTTPSGSGMFMGWPAFLSITPN  
 HC3   AALVAEYITSMLED-----RKYLPGVCVTFQNISSN  
 HC5   AALVAEYITSMLED-----HSYLPVGSVSFQNISSN

HC2A   IDEEASMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADYIKLIPI  
 KIAA   IDEEASMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADYIKLIPI  
 rat    IDEEASMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADYIKLIPI  
 HC4   IDEEASMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADYIKLIPI  
 HC1   IDEEASMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADYIKLIPI  
 HC3   IDEEASMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADYIKLIPI  
 HC5   IDEEASMEDVGMQD-----VHFNEVDLMELLEQCADGLWKAERYELIADYIKLIPI

HC2A   YEKRRD-----ITAM   ITAM   ITAM   ITAM  
 KIAA   YEKRRD-----ITAM   ITAM   ITAM   ITAM  
 rat    YEKRRD-----ITAM   ITAM   ITAM   ITAM  
 HC4   YEKRRD-----ITAM   ITAM   ITAM   ITAM  
 HC1   YEKRRD-----ITAM   ITAM   ITAM   ITAM  
 HC3   YEKRRD-----ITAM   ITAM   ITAM   ITAM  
 HC5   YEKRRD-----ITAM   ITAM   ITAM   ITAM

HC2A   -FFEDEDGKHYIYKEFKLTPLSEISORLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKFA  
 KIAA   -FFEDEDGKHYIYKEFKLTPLSEISORLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKFA  
 rat    -FFEDEDGKHYIYKEFKLTPLSEISORLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKFA  
 HC4   -FFEDEDGKHYIYKEFKLTPLSEISORLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKFA  
 HC1   -FFEDEDGKHYIYKEFKLTPLSEISORLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKFA  
 HC3   -FFEDEDGKHYIYKEFKLTPLSEISORLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKFA  
 HC5   -FFEDEDGKHYIYKEFKLTPLSEISORLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKFA

HC2A   ITAM  
 KIAA   ITAM  
 rat    ITAM  
 HC4   ITAM  
 HC1   ITAM  
 HC3   ITAM  
 HC5   ITAM

## Coiled-Coil 1

HC2A IHCFFYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLQGSV  
 KIAA IHCFFYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLQGSV  
 rat IHCFFYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLQGSV  
 HC4 SNSFFYVKKRIPINCEQQINTKPIDGATDEIKDKTAELQKLCSSSTDVDMIQKLQKLQGSV  
 HC1 SHLFFYVKKRIQVISQSSTEINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLQGSV  
 HC3 SHAFFYIKTRVNVTHKEEIIITPIEVAIDEMSKKKTQLAFATHQDPADPKMLQAVLQGSV  
 HC5 MHAFFYIKTRISVIQKEEFVITPIEVAIDEMSKKKTQLAVAINQEPADKMLQAVLQGSV

## Coiled-Coil 2

HC2A SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAIJAVNERLIKEDQLE  
 KIAA SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAIJAVNERLIKEDQLE  
 rat SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAIJAVNERLIKEDQLE  
 HC4 SVQVNAGPLAYARAFLLDNDQASKYPPKKVSELKMEFRKFIQACSIAJELNERLIKEDQVE  
 HC1 SVKVNAGMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQAIJAVNERLIKEDQLE  
 HC3 GTTVNQGFLEVAQVFLSEIPSPDKLFRHHNKLRLCFKDFTKRCEDAIRKNKSLIGPVQKE  
 HC5 GATTVNQGFLEVAQVFLAEIPADPKLYRHHNKLRLCFKDFTKRCGEAVEKNKRLITADQRE

## Coiled-Coil 2

HC2A YQEEMKANYREMAKELSEIMHEQICPLEEKT-SVLPNSLHIFNAISGTPPTSTMVHGTTSS  
 KIAA YQEEMKANYREMAKELSEIMHEQLG-----  
 rat YQEEMKANYREIRKELSDIIVERICPGEDKRATKFAHLQRHQRDNTKHSGSRVDQFILS  
 HC4 YHEGLKSNFRDMVKELSDIIEHQILQEDTMHS PWSNTHLVFCAISGTS SDRGYGSPRYA  
 HC1 YQEEELRSHYKIMLSELSTVMNEQITGRDDLK---RGVDQCTTRVISKATPALPTVSISS  
 HC3 YQRELG---KLSS-----PZ-----  
 HC5 YQEEELKKNYNKLENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCTQLSQGSZ-

## PBM

HC2A SSVY-----  
 KIAA SSVY-----  
 rat -----  
 HC4 CVTLLPHEPHVGTCTCFVMCKLRTTFRANHWFCQAQEEAMNGREKEPWTVI FNSRFYRSWGK  
 HC1 EVL-----  
 HC3 SAEY-----  
 HC5 -----

HC2A -----  
 KIAA -----  
 rat VHIFF-----  
 HC4 -----  
 HC1 -----  
 HC3 -----  
 HC5 -----

	A	B
CLASP-1	YRVAFYQQ:::GFFEEEGKEYIYKEP	
KIAA1058	FRVAFFGQAAQYQFTDSETDVEGFFEDEGKEYIYKEP	
CLASP-2		FEDEGKEYIYKEP
CLASP-6	FRVAFFGQ:::GFFEEDEGKEYIYKEP	
CLASP-4	FRVAFYQQ:::SFEEEGKEYIYKEP	
DOCK180	FAVGYGQ:::GFPTFLRGKVFIYRGKEYERRED	
DOCK2	FAVGYGQ:::GFPSFLRNKVFYIYRGKEYERRED	
DOCK3	FRVGFYGR:::KFPFFLRNKEYVCRGH	
KIAA0716	FRVGFYGR:::KFPFFLRNKEYVCRGH	
CLASP-3	FRVGFYGT:::KFGDLDEQEFVYKEP	
CONSENSUS	F V FYG	KEY K
	YF	Q F R

	C
TRG	<u>PKLTPLSEISORLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKEA</u> <u>YIQVTHVTPFFDEKE</u>
CLASP-1	PKLTGLSEISORLLKLYADKFGADNVKIIQDSNKVNPCKDLDPKYAHIQVTVTPFFEEKE
CLASP-2	PKLTPLSEISORLLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAHIQVTHVTPFFDEKE
CLASP-4	PKLTGLSEISRLVLKLYGEKFGTENVKIIQDSKVNAKELDPKYAHIQVTVYVFPFDKE
CLASP-3	PAITKLAIEISHRLGFGYGERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEPYFDTYE
KIAA0716	HDYERLEAFQQRMLNEFFHAIA-----MQHANQPDETIFQAEAAQLQIYAVTPIPEBQE
DOCK3	HDYERLEAFQQRMLSEFPQAVA-----MQHPNHPPDAIILQCCDAQLQIYAVTPIPDVVD
DOCK2	FQMLMTQFPNAEK-----MNTTSAPGDDVKNAPGQYIQCFVTQVPVLDSEHP
DOCK180	EYERREDFQMLMTQFPNAEK-----MNTTSAPGDDVKNAPGQYIQCFVTQVPVLDSEHP
CONSENSUS	L L Y
	M F
	YIQ+ V P D
	L E

	D	E
CLASP-1	RTILITSHLFFPVYKKRIQVISQSSSTELNPIEVAIDEMSRKVSELN	
TRG	RTILITAIHCFPVYKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH	
KIAA1058	RTILITAIHCFPVYKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR	
CLASP-2	RTILITAIHCFPVYKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR	
CLASP-6	RTILITAIHCFPVYKKRIPFMYQHHTDLNPIEV: HDEMSSKKVAELR	
CLASP-4	RTILITTSNSFPVYKKRIPINCEQQINLKPIDVATDEIKDKTAEQL	
CLASP-3	RTILITTSNSFPVYKTRVNVTHKEIILTPIEVAIDEMQKKTQELA	
CLASP-5	NTVLITMHAFFPYIKTRISVIQKEEFVLTPIEVAIDEMKKKTQLQA	
KIAA0716	RTSLYLVSQSLPGISRWFEVEVKREVVEMSPLENAIEVLNKNQQLK	
DOCK2	RTSFVTAYKLPGLIRWFEVVHMSQTTISPLENAIETMTSTANEKIL	
DOCK3	RTTILTLTHSLPGISRWFEVEVERRELVEVSPLENAIQVVENKNQELR	
DOCK180	RTSFVTAYKLPGLIRWFEVVHMSQTTISPLENAIETMTSTANEKIL	
CONSENSUS	RT I L F P P V + V + P+E AI+ M +L	
	L L L	I

FIG. 5B

## CLASP/DOCK MOTIF

	F				G								
CLASP-1	SLOLKLOGSVSVKVNAGPLA				YARAFLEETNAKKYEDNQV--KLLKEIFRQFADACGQALD								
TRG	KLQLKLOGSVSVQVNAGPLA				YARAFLEDDTNTKRYPDNKV--KLLKEVFRQFVEACGQALA								
KIAA1058	KLQLKLOGSVSVQVNAGPLA				YARAFLEDDTNTKRYPDNKV--KLLKEVFRQFVEACGQALA								
CLASP-2	KLQLKLOGSVSVQVNAGPLA				YARAFLEDDTNTKRYPDNKV--KLLKEVFRQFVEACGQALA								
CLASP-6	KLQLKLOGSVSVQVNAGPLA				YARAFLEDDTNTKRYPDNKV--KLLKEVFRQFVEACGQALA								
CLASP-3	MLQMVLOGSVGTTVNQGLE				VAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR								
CLASP-4	KLQLKLOGCVSVQVNAGPLA				YARAFLEDDTNTKRYPDNKV--KLLKEVFRQFVEACGQALA								
CLASP-5	MLQMVLOGSVGATVNQGLE				VAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE								
KIAA0716	PLTMCLNGVIDAAVNGGVS				RYQEAFFVKEYILSHPEDEGEKIARLRELMLEQAQIILEFGLA								
DOCK2	PLSMLLNGIVDPAVMGGF				AKYEKAFFTEEYVRDHPEDODKLTHLKDLIAWQIIPFLGAGIK								
DOCK3	LLSMCLNGVIDAAVNGGVS				RYQEAFFVKEYILSHPEDEGEKIARLRELMLEQAQIILEFGLA								
DOCK180	PLSMLLNGIVDPAVMGGF				AKYEKAFFTEEYVRDHPEDODKLTHLKDLIAWQIIPFLGAGIK								
CONSENSUS	L	M	L+G	V	VN	G	Y	AFL	+	+	P	L+	L
	L			I			V	V	F	+			I

DOCK2=KIAA0209

DOCK3=KIAA0299

CLASP2variant=KIAA1058

Fig. 5B (cont.)

2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 72  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

162 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr  
↓ ref 1.1, 1.2 and 1.3

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

462 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 4A

722 ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC 752 CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA  
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT 812 ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA  
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 1Cadherin Cleavage1 872 GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT  
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 932 GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG  
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 992 AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC  
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly  
ref 2.1 ↓

1022 1052 TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC  
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 1112 CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG  
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 1172 TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT  
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 1232 GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG  
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

1262 1292 GAG GTG GGG ACA GCC CTC CAG GAG TTC CCG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC  
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu  
ref 3.1 ↓

1322 1352 AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA  
lys asn leu leu ile lys his ser phe asp arg tyr ala ser arg ser his gln ala

1382 1412/471 AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC  
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 1472 AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC  
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

1502 1532

Fig. 6A (cont.)

CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC  
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1562

1592

AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA  
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622

1652

ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT  
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp  
ref 5.1 and 5.2

1682

1712

TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA  
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742

1772

CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT  
gln ser ser thr leu gly asn ser val arg cys asp lys leu asp gln ser glu ile

1802

1832

AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT  
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862

1892

ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC  
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1922

1952

TGC CTG CAC CAG TTC CAG TAC ATG GGC AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG  
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982

2012

GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA  
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042

2072

ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC  
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102

2132

AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT  
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2162

2192

ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC  
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2222

2252

CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG  
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2282

2312

Fig. 6A (cont.)



TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG  
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372  
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT  
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432  
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC  
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492  
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT  
ser gln leu leu tyr phe leu met arg asn phe asp tyr thr gly lys lys ser phe

2522 2552  
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC  
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612  
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC  
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672  
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC  
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732  
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG  
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792  
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG  
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 1xxxxxxxxxxxxxxx Predicted  
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC  
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA  
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972  
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA  
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu  
ref 8.1

3002 3032  
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG  
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 3092  
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT  
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu



ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962

3992

AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022

xxxxx PBM xxxxxx!

ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
met val his gly met thr ser ser ser ser val val STP

4082

4112

TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142

4172

ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202

4232

TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262

4292

GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322

4352

CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382

4412

GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

↓ ref 13.1

4442

4472

CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502

4532

GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562

4592

TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622

4652

GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682

4712

TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742

4772

ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802

TTT ACT

Flg. 6A (cont.)

## BAC sequences of Human CLASP 2

### Ref 1.1

Sequence of BAC4 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 356-375.

TTTCTACAGNGTNTACTCAGGTATGTGCTCCTTCAACAAAATTAGCAGTTGCTGCTCTG  
TGACAAAGTGTGACCATTTTGCAAGAAAGAAAAAATCCTAATGTGTTATATTACTATA  
TTTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAACCTGAAGTGCCTTATATGTA  
TTCATATAAATGACTAGTACAAGCATCATTTTGCAACAGATTTCCCTTTTCATTGGAGG  
ATCTTCTTGATGTTATTTGTACACGATCAATTTTAGTCTTAATAAGATGAGGCTGGGTG  
TGGTGGCTCACACCTGTAATCCTAGCATTTTGAGGGCCAAGGTGGGCAGATCACTTTAG  
CCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTACAAAAATAC  
NAAAATTATCCAGGCATGGTGATGTGTGCTGTAGTCCCAACTNCCTAGGAGGCTAGG  
GGTAGGGGGATTGCAAGAGGCTGGGAGGGTCAAAGCCNAANTGAGCCATTGGTNC  
ATGTCACCTGGACCCCAAGCNGGGGNGANCAAGAGCAAAGGACTNNTGTNNTTTAN  
AAAAAAAACCGGGCTACCATACNNACCAACCCNCNNACTACCCNACCTTTCCANNNT  
AAAAANAAGGCTTTGNCTTGACANAGGAAAAANCAAAATNNCC

### Ref 1.2

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 351-375.

TCTGGTTTCTACAGTGTATACTNAGGTATGTGCTCCTTNAACAAAATTAGCAGTTGCTG  
TCTGTGACAAAAGTTTGACCATTTTGCAAGAAAGAAAAAATCCTAATGTGTTATATTA  
CTATATTTTACTCTATAGATCTTTTCTAAAGAAAGAAAGTACAACCTGAAGTGCTTAT  
ATGTATTCATATAAATGACTAGTACAAGCATCATTTTGCAACAGATTTCCCTTTTCATT  
GGAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTAGTCTTAATAAGATGAGGC  
TGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGAGGGCCAAGGTGGGCAGATC  
ACTTAGCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTACA  
AAAATACAAAAAATTATCCAGGCATGGTGATGTGTGCTGTAGTCCCAGCTACCTAGGA  
GGCTAGGGTAGGGGGATTGCAAGAGGCTNGAGGTCAAGGCCCGCAGTGAGCCATGG  
TCATGTCACGTGACCCCGACGGGCCGACAGGAGCAAGACTNNTGTNTCAAAAAA  
AACAGNAACCAACANCCAACAACAACNACCTTTTCNGCAAAAANAAGCTTGCTNCA  
ANGAAACCAAAATGNCTTCTTNTTTTCCCCCN

### Ref 1.3

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is not found within this sequence. This sequence most likely represent intron sequence since this sequence matches the intron sequence found in the previous two BAC sequences.

AGNNNNCCCNCTACNCCACTTTTAACTTTTGAAAAACACAGTGTTTNTCTCAANTATGC  
GCTCCTTCACATATTAGCAGTTGCTGCTGTGACATAGTTGCACCATTTGCAAGAAG  
AAAAATCCTAAGTGTNATATCACTATATNNNTACTCTATAGATCTTNTCTAAAGAAAG  
AAAGTCAACTGATGTGCTTATATGTATNCATATAAATGACTAGTACATGCATCTTTG  
CAACAGATNTCTCCTCACATGGAGGATCTTCTNGANGNATTGCACGACGATNANTATTA  
GTCTNAATAAGATGANGCTGGTGTGGNGGTACACTGNATCTAGCATNTGGANGCATGT

Flg. 6A (cont.)

GGCAGACACTTANCCNCGGTNGAGACAGCTGTCACTGNCNAACTGTCTCTNTAAANCA  
 AANNCTCCGCGNGGNGATGGGCTGAGCCAGTCTAGNNGCTAGNTAGNGATGNNAGN  
 TGTNGCAGCNGCAGNGAGCATGNTCTGTACTGACTCATCAGGCGNCNACACGNTCTGT  
 TCNAAAACATACCAACACACACTGNCACCTNCGCAAAATGTCTNNAAANATGCTTNT  
 TTCACACNGNTNCAATCNCTATATNNTCTTCTATTCTNACGNTNNTANNATCTTN  
 CNCTGCANAAACNATNCGNCCACCTNNANNACCTTANGCTTNGTTTACGCTTATAGCTC  
 CCTACACNTNNCAGCNNTTNCNNGTGAAGGGCCNCCGAATCTACGANCATACTCTC  
 TCCGTATATNGCCTCGGTCANCGCCATCTGCTGTNTNCTCNCTNCGCNNTNANCN  
 TNCGCTATCTCTNNNCCGGATCCNCCCATATNNNNCTCTACTTANAGCGTAANNNTNT  
 NCNCCNCACTANTCAAACTTNTNCTNNAACTCTATCTNCTCCTCTACCCACTCACT  
 TACTACCTNTTACNCANTCTCCTTNCNTNTCCACTGATCTCCACATAGCTGCTNTACTC  
 GCCANTTTATCATATNCACACNCTCTACGCTNNNTNT

### Ref 2.1

Sequence of BAC4 using primer HC2S1, which spans nucleotides 1107-1126 of the cDNA. Exon sequence is underlined and represents nucleotides 1079-1097.

CTTGTATTNAAAGAGGGTCTGCAGGAAGAAGTGTGTAGTCATAAATACCTCACTGGAT  
 ATTTTATACAGGATTCTAAAAAACCTATTAGCAATAGTATGCTAGAAAATAGTCATTAGC  
 TTCTTGACCTTCTTAGAACTGCACACTCTATTGCACTGTACAGATTTTCAGGATTCGCTC  
 AGGGATTGATTTGAAAACTAAGGACACATTTCAATAAACAATGCTTCAATTGATTTTT  
 AGGGCTCCTCTACTTCAATGAAGGACTTCAGGTAGCTTATAATTACAGACACAGGCTC  
 AATACAAATAAAAAAATAGTAAGGCAGAGCTTTAAAAAAGGAAAAAGATAA  
 TTCTACCAGAGAAAGGCTACATGGTGACTTCTGTTACCAGTAACAACCCCGCACTACC  
 TTTGGGTCTCCAGGAGCAAAACAGCTAATGTAGTTGTTGATCTGCTTGAAGACAAAGC  
 CCCTGTCCATGAAGGTGAAACATCTCTGTGGAGGAAACAGCAAAAAAGTTATTTCA  
 GGTCAAACATTTGCGAAATTTGGATTCAAAGCAGGCAATTTATGCTAATAAAGTTTATC  
 CACTGACATAAAAAACATGCCTTCAACATTGCCAGAGCACCTACTCTATTNTAGTCNCN

### Ref 3.1

Sequence of BAC4 using primer C96AS, which spans nucleotides 1443-1452 of the cDNA. Exon sequence is underlined and represents nucleotides 1370-1422.

AATCAGCAGACCAAACAGAGGCAGGTAGAGGGTGGCTATCCTTGCCCTGATGGCTCTGA  
 AAAGAAGACACACATGGTAAGTTTGACCCAGGATCTGAGAACCAGCAATAAGTTGGTG  
 CTGACCATCTCCTTTATTGGATCTTCTTATAAAGACAGATATTTGATTTTAGTCCCAA  
 AATAGAGCAAAATCTTAGTGCTGTTACCATGAATTTCTAAGTGAATTTCTTTTACAC  
 CACTTAAAAATAAGGACATTATCAATGCACATTCCTTCCATTGGGGACCACTCACCTT  
 GAAGCATATCTGTCACTCAAAAAGAAATGCTTTATCAGCAGGTTCTTGAGCACAATGATGGC  
 GATCAGACGGACCTCCCGGAACCTCTGGAGGGCTGTCCCCACCTCCCTNAGTAACAGT  
 CCCAACGAAGTGGTTTCTGCAGAACTCATCTGTTAATGATGATGTAAGCTGGGAGG  
 TCTGAAATGAGGATAGAAACTACTTTGNGTTAGGAAGATGCAATGCTCTTTTGAATA  
 AAACAAACAAACCAACNAAACAAAAAATAAGACCCATCCTTNTGNATTTCAA  
 GCCCACCTTGGGTNGGTCAGAGAGATGATCAGNANTTTGGCNTTNAATGAAGAAAG  
 AAATNAAATNTCCAGGGGNTGTTCTNCTTTTAGCACANGGAGGATNTTAANTGAAA  
 ACCAATTTAAATCCAATTNAGNG

### Ref 4.1

Fig. 6A (cont.)

Sequence of BAC4 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCTCTTCTGCAAGGCTGTTCCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGCA  
TTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAAGCTAAATGGAAATC  
AAGCCAAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACCTTA  
AGGGAAATTGCTTTTATTGCACTTATTTTTCTGTTAGGAAGTTGGCTCAAGAGTTGCAT  
TCCATTACTTCACCTTTAAAGAACCCAGGTCATATACAATGAGATAAAAAAGAACTAGT  
CTGAAACATTTCAGATGTAAACATCAATTCCTTGTAGAAAACACCTTTGATCGCTAAA  
GACTAAATCCATACCTGTTTTCAGAAATGTGATAGAATGAAGACTTAAAAAAATTTAAAG  
ATAAATCCACCTACAACATCAAAATCACAAAATTAACCCACACAACAACTTGTAGCA  
TTCAAACCTGGTAATAAAACACTGAGGAGCCTACCCAACTCTGAGGGGTGTCATGGGGTA  
TTTTAAATTTTCGAGGAGAACACAGTGATATGTGACCTCAGCCAGAAGCTGCTGTTTNA  
GCAGCAGGTTGGTGCTATGCTCCTTTTTGAAGACATATTTGTGAAGCTGGGTATTTGG  
GGGGCTGCTTATGATAAAAANGGCAAGGTTNTTCAATGNAGGGGN

#### Ref 4.2

Sequence of BAC26 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCTTTCTGGAAGGCTGTTACCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGC  
ATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAAGCTAAATGGAAAT  
CAAGCCAAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACCTT  
AAGGAAATTTGCTTTTATTGCACTTATTTTTCTGTTAGGAAGTTGGCTCAAGAGTTGC  
ATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAAGAACTA  
GTCTGAAACATTTCAGATGTAAACATCAATTCCTTGTAGAAAACACCTTTGATCGCTA  
AAGATAAAATGCATACCTGTTTCAGAAATGTGATAGAATGAAGACTTAAAAAAATTTAAA  
AGATAAATCCACCTACAACATCAAAATCACAAAATTAACCNCAACAACAACTTGTAG  
CATTCAAACTGGTAATAAAACACTGAGGAGCCTACCCAACTTTGAGGGGTGTCATGG  
GGTNTTTTTTAAATTTTTCGNGGGANANCCCACTGNTATGGTGACCTTCACCCAAGAAAGC  
TTGTTTGTTTNACCAAGCNAGGTTGNNCTNTGCTCCTTTTTAGAAANACNNATATTTNNN  
AAATNCTGGNTTTTTTNNNGGGCCCCCTNCNTTNTT

#### Ref 5.1

Sequence of BAC4 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1724-1736.

TTCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTATAATCAATGGATT  
TCGCCAAAGCTAAACGTACTTCATGTTCTAGTGCCCTTTAAAGTTGACCTTTGTTTTTT  
ATAAACACCCGGCTGACCTGAGTGAGTGATGAGAGCTTTAAGGTTGGGGCCCATTC  
CTTGAAGTGCTCTGATTCTCTGTTTCCAGTACCTCAGATCCTGGGCAGGGTTTGCAGTGG  
AGCGCTTGTAGTGAATGGCTCTGGTGGGTTGAACGGGGAGGGACTCAAAATGCTGCC  
ATCTCAATTTCTGTAGTCTTTTATTATTATTATTATTTGAGACAGAGTCTCGCTCT  
GTGCGCCAGGCTGGAGTACAGCGGCACGATCTCAATTNACTGCAACCTCCGCTCC:TG  
GGTTCAAACGACTCCTCTGCCTCAGCCTCCCCAGCAGC:TGGGACCACAGGCACAAGCC  
ACCAACGCCCGGCTAAATTTTTGTNTTTTTAGTA:GAGAT:GGGGTTTCAACCATTTTGGC  
CAGGCTGGGCTCAAACCTCCTGACC:TCGTCAATCCGCNCCCTCGGNCNTNCCAAAGTGCTT  
GGGATTNCAGGCGTGTAGCCCACTTACACCTNNGGGCAATTCCTGTNAGTCTTTTTTAC  
CAGAGACACCATCATTCAACACAGCTTTTCCACCCACAA

Fig. 6A (cont.)

#### Ref 5.2

Sequence of BAC26 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1712-1736.

TGAGAAAGAGCAATTTCTTGGATAAGGTAATTGCTTTTACCCCAACACAAATGTTTCTTAT  
AATCAATGGATTTAGCCCAAAGTAAACGTAACCTCATGTTCTAGTGCCTTTAAGTGTGA  
CCTTTTGTTTTTTCTAAACCAACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGG  
TTGGGGCCCATTCCTTGAAGTGCTCTGATTCCCTGTTTCCAGTACCTCAGATCCTGGGCA  
GGGTTTGCACTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTGAACGGGGAGGGACT  
CAAAATGCTGCCCATCTCAATTTCTGTAGTCTTTTATTTATTTATTTATTTTGGAGAC  
AGAGTCTCGCTCTGTGCCCAAGGCTGGAGTACAGCGGCACGATCTCAATTCATCTGCAA  
CCTCCGNTCCCTGGGTTCAAACGACTCCTCTGNCNAGNCTCCCAGCAGCCTGGGAA  
CCACAGGCTCANGCCACCACGCCCGGCTAATTNTTGAATTTTNAAGTAANAAATTGGG  
GGTTCTACCATNTTTGGCCCAAGNCTTGGGCCTAAAAACCTTNCNACCNTCGNCATT  
NCNCCCNACCNCTGGGNCNTNCTCAAANGNGCTTGGGGATTANCANNGGCNTTAACC  
CCCCNTATCACCGTGGNCCTTAATTT

#### Ref 6.1

Sequence of BAC4 using primer C2S7, which spans nucleotides 1918-1937 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S7 is intron sequence.

NAGNNGGGGTTTINAGNCGTTTGAAGCCTGNNACGNGGTGNGTGCTNGAACTCTGTGGG  
CTTTCAGGTACTGGGGTATCTGGGAGCCTGCTGTTTGCATCTGCTAGTGCATCAGACCAG  
GGCTTTTCTCCCTGTAGCTGCTACTTATACACATAGCTTCAACTGAGATGATTCTCCA  
GACAACTGATGCAGAGCAGCAAAAGCTTCTGCCGTTCTCCCTCTCAGGAGTGTCTCCT  
TCTTTGGAAAGAGATCATAGGGGCTAGATTGTAATGAAGTGAGGGCTCAGTGCTTGA  
GCACATCCGGTAAAAGTTCCTCAATATATTGGTCATAAAGTTTCTCATTCTTTATAGCAGT  
TAATTTCTCTGGCTCATGAGTTTTCTTAGTTTTAATCTGACTTTTAAATTAATGTCTCCA  
GCACAGTCATATCCCCAGGGCAAACTCAAAGGCATGAGAGGCCAGACTCGGGTCTGT  
GTCATAGCAACCCCTGTCTAGGGCCTTGGTCCCTGCCCTCCGCTTGTGTGCTGTGGCGCA  
GGTCCTATGGGCCCTTAGGAAACAGGACCACCTGTGCGACCCCTACAGAGACCAGC  
CAAGTTTGACATTAGATCACCGTAGCAATGTNTGCAAAATCCAGTTTCTTGCTAAAAACA  
GGTTAAGCCTTGCAGCCACTTTATCTGTAACCTGGCNGAGGTTTTGACATAAAAA

#### Ref 7.1

Sequence of BAC4 using primer C2S8, which spans nucleotides 2143-2162 of the cDNA. Exon sequence is underlined and represents nucleotides 2182-2219.

CTCTCGACACGCTGTTTCTATTAACATTGGCGTTTAAAGGTTTGTATCAATTTGCTGTTG  
NGGTTCTAGTTTTACCTTTACATTCATTCTGCTTGGTAAGCTCAGTGAGCACAACATTA  
CTATGTTGCATTTTACTTCAGCAATTATTTTGTCCCTGTAAGGAAACCATTAATCTTT  
AAATTCCTTTAATGAAATCAATCCACAGTGAATGGCTTGAATGCCCTGAAATAAAATTT  
AACTGGTCAGTGTGTGCTGCGCGCTTGGGTATGGTGGAACACCGTCTCTGGAGGCAG  
TTAACTCTTGGCTCGAACCTTGAGGATGGTGAATATAGGCACCTAATCAGGCATTCTG  
CCTTGAATATCTTTAAATATATCCAAATGTTATAGCGTTTAATTAGATTTTATGTAGAA  
AGGAGCAATAAACACAAGACACATGTTTTTCAGTTTTTATCTGTTACTGCATTAATGA

TAAAAACGTTTTGGAGATAGAAAAATGAAAGGGGTTTTTTTTTGTCTTGTTTTAAAGTT  
 TTAGCAAATAATATTCAAGTAGGTGGAGATGGACTCTTCACCACCTCTCCTGTTTTTAGG  
 AACCCCAATACTTTTTTCATTCTTGCTAAATGATTACTTCCATTCTAGCATAGAAAAAGGA  
 GAAAATTGGAATGAGTGTTTATAT

#### Ref 8.1

Sequence of BAC4 using primer C2S9, which spans nucleotides 2992-3011 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

CGCTTTNAAATNCCAGCCGCTACTGCGGGGCGNTNAAATCGAAACGTTGTINTCTGT  
 GATGCCCTGGCTCTGATTGTGTGGGATTGGTCATCAGTGGCGGTTGGCAGNTGGGGTTCA  
 TGGAAAGCGGCCATGGGGACTGATGGCAGGCCCTTGGATTGCCACCGCAGAGCCTGGCA  
 GTGTCTTTGGTCTGCATTCTCAACGGCGAAAGTCTCATTTACCTCACGTGTTATCTCTTG  
 GAAAGCATCTCCTTTAGCGGGCTGTGTCTACCCTTCCATCCTCTCGTCCAAACTCCCCCTC  
 CTCTCTGTTCTGTCTCCTTCCCACCTCTTCTCCCCAGTTCTTCTTCTATGTTCTCTCCT  
 CAGTGGTTTTCTCTCCTCTGTTTGACTTTCCAAGGTCAATTTGACTGTTCTCTGCTCCCAA  
 CTCACAAAGATACTAAAACTCACCTAACCACTCTTCTTCTTCTTAATGAAAGAATGTT  
 TTCAGTCCATCCCAAATTTGTGTGGACTTCACAAACCTTCTCTAAAATGGAGCCTTTTTCT  
 CTTCCTACTCTTGACTAGNTGGTAAACGCTCCATGTTCTTGCCAGAAGTCCCTGGTGA  
 GCGTCACTCCTCCACTTTCTGTGCAGAACCAAGCCTCCTAGAAAACTCCTTTGCANC  
 TGAGTGGGTTGGGACACGCCCTTTNTTGGG

#### Ref 9.1

Sequence of BAC4 using primer C2AS10, which spans nucleotides 3276-3295 of the cDNA. Exon sequence is underlined and represents nucleotides 3147-3234.

TTTANACCNATNTATCCGNGTCAGTTANAGGAGTCTCTGAGAAAATTTCCGACAGCGGT  
GTGAGTTTGGGTTCCTTGTAAATATACTCCTTTCCATCTTTCATCTTCAAAGAATCCCTGT  
 GACATAAAGCACAAATTAGAGCTATCCCTGAACGTAAGCCCAGGGCTTACCACCTAGGA  
 AGCGTTCTTTTATTACAAGGGGGGAAAAAAGGAATGGGTCTAAAAATCCAGCTGAAAT  
 GGGCTTTCTGAATGAGAAAGAAAAATGCTAATAACATGAAGTCTAGGTGCAAAGGTAAA  
 GGAAAAACACAACATTGCAAACTTATTCAAGAATGCAGTCAATTAAGTGTGAGTGAA  
 TGAAAGATTITGGATACAAGACTAAGCTGTCCCAGGGAAGTCTAATGGGAGTCAAGCC  
 TGTTTCACTTTCCCAAGAAGCAGAACTCACTANAAAAATGATGAGCAGCCACGACAGG  
 CAGGCTCAGAAGTGGACATGCTCCCTTCTCCTGATGGCTNCCATGCACACAGGATTTT  
 ATGGCATGAAGTGAAGCGTTTGGGGGTCTGGAGTAAGTTTAGTAAAAAGTTAGGTAAAG  
 CTTGTATAAAATGTATTTTGCCTTACCCTGATGAGAAAAAATATTNAGACCTGGTA  
 GCTTCAATATTCAAGAAAAATATTTTTCATNTCACCCG

#### Ref 10.1

Sequence of BAC4 using primer C2S11, which spans nucleotides 3167-3186 of the cDNA. Exon sequence is underlined and represents nucleotides 3231-3296.

NGNANGTGGAGCCNCGANCCAGGGACAATCTNAAACCTNCTTAAACTGTACTCGGATNA  
ATTGGTTCTGAAAAATGTCAAAATGATACAGGATTCTGGCAAGGTATTGACCATGTTTG  
 GANAAGTTTCATAGCAATGTAATGTTGTGATNCGATTACATATNATATATTTTTAAATG  
 TNTATAGAAAAAACACANGAAAAATATTAAGGATTGTTGGCCCGTGAGTGGCAGGTG  
 TATNTTCTTCTGATCCTTTAGNGCTTTCCATTACATGCNTGACATTAAAAAANCTTTA

Flg. 6A (cont.)



TCGCCTAATTTTGAACATCTAATTTTACAAAATAATTAACCGTNTGGCCANGNATAT  
 TNTCATTTTTAGGNCCAGCTATTTAGAAACTCTGCANAAATGAGGGGCTGTGGCTTNC  
 CTNCCTNNACTTGNCCTCTTTTCNNGNATGTACCACATGAACCTTGNCNCCTCTTTTCNNC  
 TNACCGGGTGGCATGTTANAGGACAGGTTGAAACCNCANTNNGGCGNGGANTTNGGTN  
 NAATTGGGACACAATGGTACNANGCTCTATNGGAATNGAAACTCTCCCNACNNNCNGT  
 GNCCNTGGGGAAAATGNGNCNNATTCTATTTT

#### Ref 11.1

Sequence of BAC4 using primer C2S12, which spans nucleotides 3474-3493 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

AGNANNGTNNNGCAGCTGCANNCTGGAACCCANAGGCCGANGGGCACGAGCCNNGGA  
 CACGCTCGGCAAGAGCTGTCCAGAGGGATTGAGAAGCTTCAGGACTGGAAGGGTCTT  
 TCGAGCTCAGTTAGCCACCCCCACACCCATTTCAGTTTCACATTTATCTAGTGCTTCCTT  
 TTGAATACTTGGGATGTTTTCTGTTGATCTGTGGCACTTCCTTCTCCACAAGACCAG  
 AAGCTCATATCCAATCTAAGGTCACTTACCCTTCTGAGAATCTGATGAAAAATGGCGTG  
 CTTATGTGCTTAGATGCTTTTGCACACAGTCTAAGGTGACTTATGGACTCCAGGTCCAG  
 CAGCCACACCCAGTCTGGTCTCCGACAGGAGGGGACCCGTCTTCACACACCTGTCT  
 CAGGTTCTAGCATTTGGGCTGCTTCAGCGGTCTCAGGCTGTGAGTAAATGGGATGTGAG  
 CTTGGATGCGCCCAACGCTGTTGNCNCCCGGGGGCTTGCCACAGCTGGCCACTTNGAAAT  
 GCCTCCTTTTGCCACAGAAAGCTCACTGCATTTCAATGGGGNTTNTCCACGAAGTTTCA  
 CTTTANGGG

#### Ref 12.1

Sequence of BAC4 using primer C2S13, which spans nucleotides 3645-3664 of the cDNA. Exon sequence is underlined and represents nucleotides 3683-3699.

AGNAAGGTNNCTCANTNAANNCAGCGTGAGNGTTCAGGTGAGCCAGGCACAGCAGGC  
CGGAGGGCAGCAGGGGACGTCCTTGCCCCGTGGGTGACTTGAGAGTCTGTTTCCACTAAC  
AAGGTCTACTTGAGAGCCTCGGTTTACCAAGTGATCCCTGCTCCCTTCCCCAACGTNT  
GTGACATTTCTCTGATATCAGAGGGGGAGGAAACCTCATGATCCCTGCCCCCCGCC  
ATGAGGACTGACTGTGGGGACAAAGAGCCAGATCTCATAGACTACCCTGATTTGTGAG  
TATTTGGGGAATTCTGGGTGCCTGATTAGAAGCATCAAGACTCTTCTAAATNCAAGA  
AGTGTGGAGAGCAGTAGATTTTCTATAAAACTGGTGTTGCTGGTTTCTATGAAATTG  
GATCCAAAAAAGTCTTAAGTTTACCCTCTTAATGGNATCTTTTGAATTAATGGAATTC  
ATTATTTTAATATAGCCCAATCAATCCAATTTTTCTTATTGGTAGCATTTTTATGTTCTC  
TTTAAAAAAATCTTGGNCTACCTCCAAAATTTACAGATGTTCTCCTAGGGTTTTCTCTC  
TTTTGTTCAAGCATCCCATCAANGTCTTGACGTCCATTCTGGGG

#### Ref 13.1

Sequence of BAC4 using primer C2S14, which spans nucleotides 4289-4308 of the cDNA. Exon sequence is underlined and represents nucleotides 4321-4448.

GACTTANATTTATCTCTCTTGACAGTAGTGTGAGAATAGATGGCCCTACAGAAAAA  
AGGTTCTGGGATCTACATGGCAGGGGAGGGCTGCAGCTGACATTGATGCTTGGGGACCT  
TTTGCTCGAGGGCTGAGCTGGAAAAATCTTGAAAAATATTTTTTTTCTGTGGCACATTC  
AGGTTGAATACAAGAACTATTTTTGTGACTATGTTTTGATGACCTAAGGGAAGTACC  
ATTGTAATTTTTGTACCANTGAACCANGAGATTAAAGTGCTTTATATTCATTTCCTTGC

Fig. 1a (cont.)

ATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAACTAGTCAAGCANTT  
TAGAACCAAAGGCCTATNTTNATAACCGCAACTATGCTNAAAAGNACAAAAGTAGTACA  
GNATATTGNTATGTACATATCATTTGGTAATACACNCCNGGCNTTCTGTACATATATGT  
ATTACATTTCTACNTTTTTAATACTCCCNTGGGCTTATGCCNTTAAGGTTAANTTGNAT  
AAATTTNGGCTGTTCCNGTNTATNACNATACNCTTT

Ref 14.1

Sequence of BAC4 using primer C2AS15, which spans nucleotides 4680-4700 of the cDNA. Exon sequence is underlined and represents nucleotides 4660-4683.

ATGAGAATGTAATACATATATGTACAGAATGCCAGGACTGTATTAACAATGATATGTA  
CATAACAATATACTGTACTACTTTGTACTTTTCAGCATAGTTGCGGTTATTAATATAGG  
CCTTTGGTTCTAAACTGCTTGACTAGTTTTAAGCTCACATAATTCCCTTAAGCTTTCATAT  
TTTCTTAAATGCAAGGAAATGAATATAAAAGCACTAAATCTCCTGGTTCAGTGGTACAA  
AAATTACAATGGTCAGTTCCTTAGGTCATCAAAAAGTACACAAAAATAGTTCTTGT  
ATTCAACCTGAATGTGCCACAGGAAAAAATAATTTTCAAGATTTTCCAGCTCAGC  
CTCGAGGCAAAAAGCCCCCAGGCATCAATGTTCAGNCGAGCCCTCCTGCCATGTAGATC  
CCAGAACCTTTTTTTCTGTAGGCCATCTATTCTAACACTACTCTGCAGGGAGAATAAA  
ATCTAAAGNCCAGCTCAAGAGTGCTACCAACACCTTTGTTAAGACACAATGAAAACTTT  
GGATATTGGCAGGNGAGATTTAAAAAATGTGCCCTTTCTTACCCTCCTATAGNA  
AAGTCTGGTTAAGAAATAACCGTTGGTCTTTATTTTCTTTTNTTCCCTTCCCTTGGG  
NCITCCTGGGGCTCGG

Fig. 6A (cont.)

HC2A  
KIAA ASGNLDKVNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD  
rat  
HC4  
HC1  
HC3  
HC5

HC2A  
KIAA FPNYVNSSYIPTKQFETCSKTPTTFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYKDSQ  
rat  
HC4  
HC1  
HC3  
HC5

HC2A  
KIAA -----VLHHHQNPFEFYDEIK  
rat KSAKARNIAICTEFKSDSEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPFEFYDEIK  
HC4  
HC1  
HC3  
HC5

HC2A  
KIAA IELPTQLHEKHLLLTFFHVSCDSSKSGSTKKRDVVETQVGYSWLPLLKDGRRVVTSEQHI  
rat IELPTQLHEKHLLLTFFHVSCDSSKSGSTKKRDVVETQVGYSWLPLLKDGRRVVTSEQHI  
HC4  
HC1  
HC3  
HC5

HC2A  
KIAA PVSANLPSGYLGYOELGMRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC  
rat PVSANLPSGYLGYOELGMRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC  
HC4  
HC1  
HC3  
HC5 -----GPGPARSTVSISLISNSARV

HC2A  
KIAA OKTESGAQALGNELVKYLSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV  
rat OKTESGAQALGNELVKYLSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV  
HC4 -----MEIQVLIIRFLSVILMQLFWLFPNMIHEDDVPISCPMV  
HC1 -----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV  
HC3 NRSRSLSNSNPDISGTPSPDDEVRSIIGSKGLDRSNSWVNTGGFKAAPWGSNFPSPAES  
HC5

Fig. 6B(cont.)

HC2A I IHVVAQCK A ESHLSRVKYAYKAEPYVASEYKTVHEEL...HTTILKPSADFLTSN  
 KIAA I IHVVAQCHEEGLESHLSRVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN  
 rat  
 HC4 LFHIVSKCHEEGLDSYLSFFIKYSRFPKPSAPOPLIHETLATMMLIALLQKQADFLAIN  
 HC1 LPDI VAKCHEEQLDHSVQSYIKFVFKTR---ACKERFVHEDLAKNVTGLLK-SNDSPTVK  
 HC3 TQAMDRSCNRMSSTHETSSFLQTLTGRLP---TKKL FHEELALQWVCSG--SVR---E  
 HC5

Cadherin  
 Cleavage

HC2A KLLRYSWFFFDVLIKSMAQHLIENSKVLLRNQRFPPASYHHAETVVMMLMPHITQKFGD  
 KIAA KLLKYSWFFFDVLIKSMAQHLIENSKVLLRNQRFPPASYHHAETVVMMLMPHITQKFRD  
 rat  
 HC4 KLLKYSWFFFEI IAKSMATYLLLENKIKLTHGQRFPPKAYHHAHSLFLAIT-IVESQYAE  
 HC1 HVLKHSWFFFAI ILSMAQHLIDTNKIQLERPORFPESYQNELDNLMVLSHDVWIKYKD  
 HC3 SALQQAFFFEFLMVKSMVHHLYFNDKLEAERKSFFPFMFDDIAALVSTIASDIVSRFOK  
 HC5

6.1  
 1.1/1.2/2.1/2.2

HC2A NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL  
 KIAA NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL  
 rat  
 HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL  
 HC1 ALEETRATHSVARFLKRCFTFMDRGCVFQMVN---NYIS--MFSSGDLTKLQCYKFDL  
 HC3 DTEMVERLNTSLAFLNLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPVLVLSRLDLF  
 HC5

2.1

7.1  
 3.1 / 3.2

HC2A RVVCNHEHYIPLNLPM---PFGKGRIQR-----YQDLQL---DYSLTDEF  
 KIAA RVVCNHEHYIPLNLPM---PFGKGRIQR-----YQDLQL---DYSLTDEF  
 rat  
 HC4 QTICNHEHYIPLNLPM---AFAPKQLQR-----VQDSNL---EYSLDSEY  
 HC1 QEVQCHENFTPLCLPIRSANIPDPLTPSES-----TQELHASDMPESYVSTNEF  
 HC3 RIICSHHYVTLNLPCSLTLPSPASPSPVSSATPQSSGFTNVQDKIANMFELS--VPF  
 HC5 -----MNADTAPTSPCPSIS-----SQNSSCSSFPQDKIASMFDRTSRVPA

4.1 / 4.2

HC2A CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 KIAA CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 rat  
 HC4 CKRHFLVGLLLRETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYOHKNQQAQIAQ  
 HC1 LYMLFLGMLLDNMPRIYKDLYPFTVNTSNQSSRDDLSNNGGFQSQTAIKHANSVDTSFS  
 HC3 RQOHYLAGVLVLTAVILDPAEGLFGLHKKVIMNMVNLSSHSDPRYSDFQIKARVAM  
 HC5 SSTSSPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKEPVVKIAA

3.1

8.1

HC2A LYLFLGILLIENVQRINVRDVSPPFVNAG-MTVKDESALPAVNPLVTPQKSGTLDNSLH  
 KIAA LYLFLGILLIENVQRINVRDVSPPFVNAG-MTVKDESALPAVNPLVTPQKSGTLDNSLH  
 rat  
 HC4 LYLFPFGILLIENIQRAGRDITYSCAAMPENSASRDEFPGC-----FTSP--AN--RGSLS  
 HC1 LYMLFLGMLLDNMPRIYKDLYPFTVNTSNQSSRDDLSNNGGFQSQTAIKHANSVDTSFS  
 HC3 LYLFLGIIIMETVPQLYDFTETHNQRGFICATDDYSE-----SG--SMIS  
 HC5 LYLFLVGIIIDALPOLCDDFTVADTRRYR---TSSGDEEQE-----GA--GAIT

9.1

4.1 / 4.2

HC2A KDLGAIISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNLSDKHQSS  
 KIAA KDLGAIISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNLSDKHQSS  
 rat  
 HC4 TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQNGTEN-----TRQS  
 HC1 KDVLNSIAPFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTONCEKIPRL  
 HC3 QTVMALAGTSVPQ-----LTRPGSFLTSTSGRQHT-----  
 HC5 QNVALAAGNNFN-----LKTSG-IVLSSLEYKQYN-----

5.1 / 5.2

10.1

3.1

2.1

HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFTTISEVCL	
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFTTISEVCL	
rat		
HC4	STRSVSQYNRLDQYEIRSLMCFYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL	
HC1	ALIGSTLRFDRLDQETRSLMCFLHIMKTISETLIAYWQ-RAPSPPEVSDFFSIIIVCL	11.1 / 11.2
HC3	-----TFSAESSRSLICLLWLKN-ADETVLQKWFTDLVQLNRLDLLYLVCV	
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKIADLPSTQLNRILLDLFICV	
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRRTGMM	6.1
KIAA	HQFQYMGKRYIAR-----TGMM	
rat		
HC4	FHFYMGKRNRIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM	
HC1	QNFYRLGKRNIIRKIAAAF--KFVQSTQNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK	
HC3	SCFEYKQKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV	
HC5	LCFEYKQKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGARGEMM	
HC2A	HARLQQL-----GSLDNS-----LTFNHSGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL-----GSLDNS-----LTFNHSGHSDADVLHQSLLEANIATEVC	
rat		
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTTEADIHQALLEGNTATEVS	
HC1	QHRSQTLPIIRGK-----NALSNPKL-----LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC	12.1 / 12.2
HC3	RRSRGQLERSPSGAFSGQENLRWRKDMTHWRQNETKLDKSRAEIEHEALI DGNLEATEAN	6.1 / 6.2
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEAALISGNLEATEAH	
HC2A	LTALDTLSLFTLAFKQQLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSIIY	7.1
KIAA	LTALDTLSLFTLAFKQQLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSIIY	
rat	-----KLSRGHSPMLKKVFDVYLCFLQKHQSEMAKKNVFTALRSIIY	
HC4	LTVLDTISFFTQCFTKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS	
HC1	LTILDLSLFTQTHORQLQCCQCSNLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVC	13.1
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHLSMACNQSAVYLQHCFAATORALVS	
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRLVNSLNCDSQSTYTLTHCFATRALIA	3.1
HC2A	KFPSTFYEGRADMCALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSEFVRTH	
KIAA	KFPSTFYEGRADMCALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSEFVRTH	
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSEFVRTH	
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCTSKISSIRTEASALLYLLMRNNFEYTKRKTFLRTH	
HC1	KFPSSAFTQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLLMRNNFEENKQKSIVRSH	
HC3	KFPPELLFEETEQCADICLRLLRHCCSSSIGTIRSHPSASLYLLMRQNFEGN--NFARVK	7.1 / 7.2
HC5	KFGDLLFEFEEVEQCFLCHQVLHHCSSSSMDVTRSQCATLYLLMRFPGATS--NFARVK	
HC2A	LQVIISVSQLIADVVGIGETRFQOQSLSIINNANSRDLIKHTSFSSDVKDLTKRIRTVLM	
KIAA	LQVIISVSQLIADVVGIGETRFQOQSLSIINNANSRDLIKHTSFSSDVKDLTKRIRTVLM	
rat	LQVIISVSQLIADVVGIGETRFQOQSLSIINNANSRDLIKHTSFSSDVKDLTKRIRTVLM	
HC4	LQVIISVSQLIADVALSGGSRFQESLFTINNANSRDLARAFPAEVKDLTKRIRTVLM	
HC1	LQIKAVVSQLIAD-AGIGGSRFQHSLATNNFANGDKQMKQBNFPAEVKDLTKRIRTVLM	14.1 / 14.2 / 15.1
HC3	MQVPMSSLSLVGTSQNFNEEFLRRSLKTIITYAEEDLELRETTFPDQVDQVLVFNHMLS	
HC5	MQVTHSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFFPTQVEELLGNLSILY	



## Coiled-Coil 1

HC2A IHCFPYVKRIPVMYQHHTDLNHEIVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV  
 KIAA IHCFPYVKRIPVMYQHHTDLNHEIVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV  
 rat IHCFPYVKRIPVMYQHHTDLNHEIVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV  
 HC4 SNSFPYVKRIPVMYQHHTDLNHEIVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV  
 HC1 SHLFPYVKRIPVMYQHHTDLNHEIVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV  
 HC3 SHAFFPYIKTRVNVTHKEEIIILTHEIVAIEDMQKKTQELAFATHQDPADPKMLQMVLOGSV  
 HC5 MHAFFPYIKTRVNVTHKEEIIILTHEIVAIEDMQKKTQELAFATHQDPADPKMLQMVLOGSV

11.1

## Coiled-Coil 2

HC2A SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGOALAVNERLIKEDQLE  
 KIAA SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGOALAVNERLIKEDQLE  
 rat SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGOALAVNERLIKEDQLE  
 HC4 SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGOALAVNERLIKEDQLE  
 HC1 SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGOALDVNERLIKEDQLE  
 HC3 GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRNKSLIGPVQKE  
 HC5 GATVNGPPEVAQVFLSEIPADPKLYRHHNKLRLCFKEFIMRCGEAEKNKRLITADQRE

11.1 / 12.1

## Coiled-Coil 2

HC2A YQEEMKANYREMAKELSEIMHEQILPLEEKTSS-VLPNSLHIFNAISGTPSTVMHGMTSS  
 KIAA YQEEMKANYREMAKELSEIMHEQILPLEEKTSS-VLPNSLHIFNAISGTPSTVMHGMTSS  
 rat YQEEMKANYREMAKELSEIMHEQILPLEEKTSS-VLPNSLHIFNAISGTPSTVMHGMTSS  
 HC4 YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFCASIGTSSDRGEPFRYA  
 HC1 YQEELRSHYKMDLSELSTVMNEQILGRDDLK---RGVDQCTCRVISKATPALPTVSIS  
 HC3 YQRELG---KLSS---PZ  
 HC5 YQOELKKNYNKLENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-

19.1

## PEM

SSVV3

HC2A  
 KIAA  
 rat  
 HC4  
 HC1  
 HC3  
 HC5

CVTLPHPEPHVGTCTVMCKLRTTFRANHWFCQAQEEAMNGNGREKEPWTVIENSFRYRSWGG

## EVL

SAEV3

HC2A  
 KIAA  
 rat  
 HC4  
 HC1  
 HC3  
 HC5

-----  
 -----  
 VHIIF  
 -----  
 -----  
 -----

HinDIII  
Eco RI



← ~ 4.5 kb

← ~ 1.85 kb

genomic DNA

Pst I  
Eco RI



← ~ 4.5 kb

← ~ 1.85 kb

BAC 6 DNA

Fig. 7



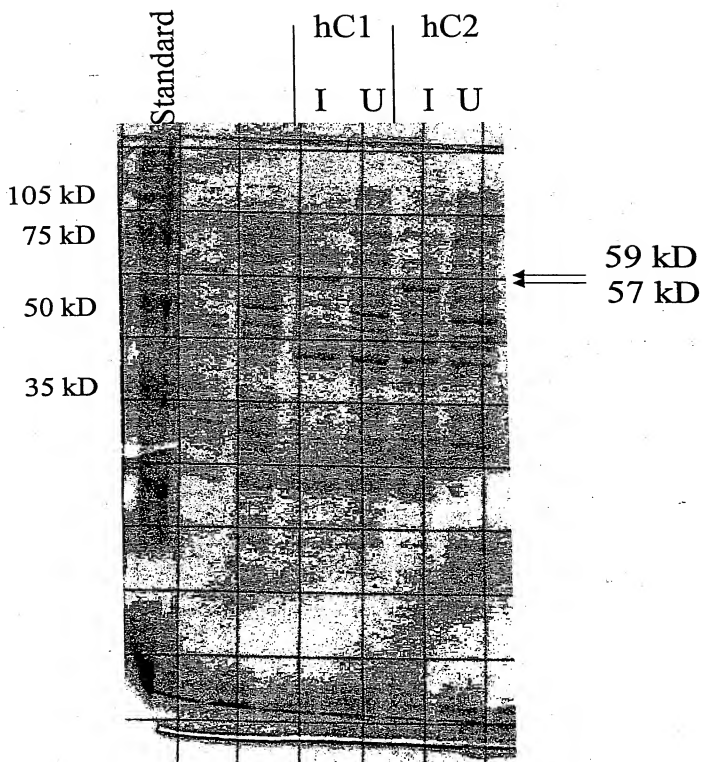


Fig. 8

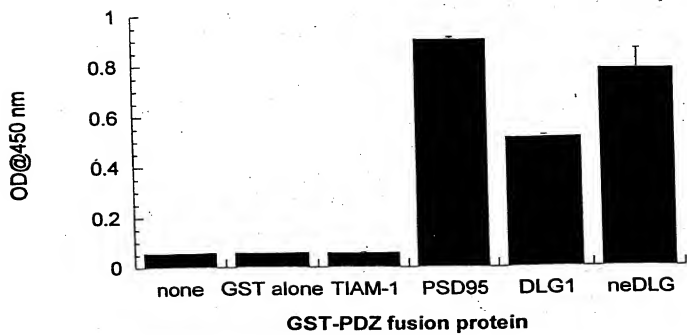


Fig. 9A

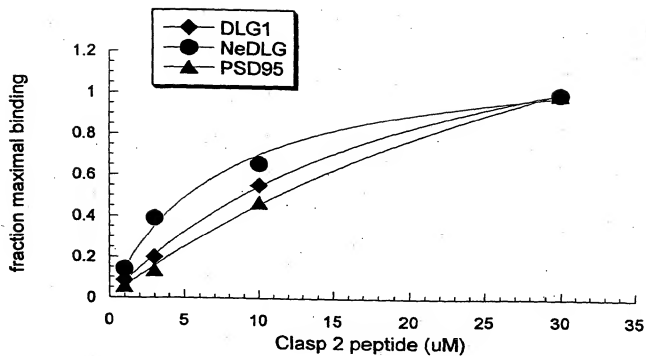


FIG. 9B

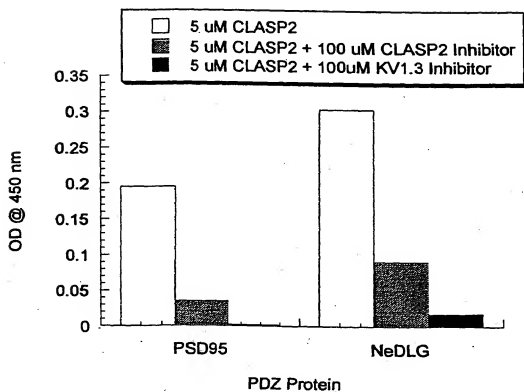


Fig. 9C

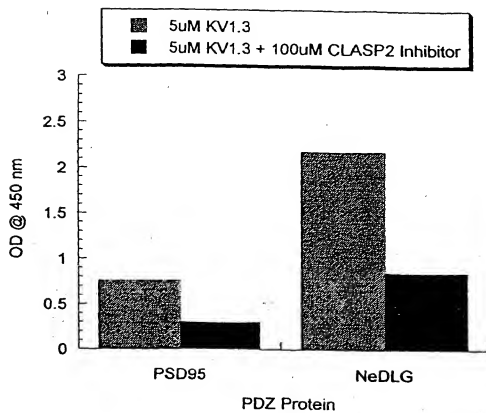


FIG. 9D

	10	20	30	40	50	60	70	80
1	AATTTGAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCTCCGCTTC	GAGGTGGAAG	GTATCGGATA	GCTTGATATC
81	GAATTCGGCA	CGAGTTTTC	ACCATCACCA	AAACCCGAGA	AGATTGAAGT	AGAGTTGACC	AGCTCAGCTGC	160
161	ATGAAAGACA	CCACCTGTGT	CTCACTATCT	TCCAATTCAG	CTGTGACCAAC	TCAAGTAAAG	GAAGCAGGAT	240
241	GTGTGTTGAA	CCCAAGTGTG	CTACTCTCGG	CTTCCCTCTC	TGAAGAACCGG	ANGGCTGTGT	ACAAGCGAGG	320
321	GCTCTGCGGG	ACCACTTCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAAGCA	TTATGTGCTG	400
401	GGGTAGATGT	AGGCAAGCCA	CTGGTGAATA	TTTCCACTCA	TTCTGTTTCT	ACAGGGATAT	TCCAGGATCAG	480
481	ATTTTTCCTA	AGGCTCTCAG	AGAGTGAAGT	CTGGAGCCCA	AGCCTTAGGA	ACAGCAATAC	TAAAGTACTCT	560
561	CATGCGATGT	AAGGCCAGCT	GATATGCGC	TCTTGCCGCA	CTATCTTAAA	CCAGCTGTCT	CGAGTCTCTA	640
641	ACAGGAGGAA	GTCCGCGTTA	ACGTGACTCG	GGTCATTAT	CATGTGTGCT	CCAGTGTGCA	ACAGGAAGGA	720
721	ACTTGAAGCT	ATATGTTAAG	TACGGGTATA	AGGCTGATAT	ATATGTTGCC	TCTGANTAGC	AGACAGTCCA	800
801	ACCAATATCC	TGACCAACAGT	TCTCAAGCCT	TCTGCCGATT	TCTCTACCAG	CAACAACATA	CTGAGGTACT	880
881	CTTTGTGTTA	TGATCAAAAT	CTATGGCTCA	CGATTTGATA	GAGAACTCCA	AGGTTAAGTT	GCTGCGAAC	960
961	CTGATCTCTA	TCATCATGCA	GGGGAAGCCG	TGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	1040
1041	GAGGCATCTA	AGAACGCCGA	TCATAGCTCT	TGCTCTTTCA	TCAGAGATGT	TTTCACTCTC	ATGGACAGGG	1120
1121	CAGGCATCTA	AACCACTACA	TATAGCTGTT	TGCTCTTTCA	GACCCAGAGA	CCCTCTTTGA	ATACACATTT	1200
1201	GTGTAGTTGT	CAACATAGAA	CATTATATTC	CGTTGATGGA	ACCAATGCCA	TTTGGAAAGG	CGAGGATTTA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTGTGCA	GAACCACTIT	CTGTGTGAGG	GAAGAGGTGG	1360
1361	GACAGCCCTC	CAGGAGTCTT	GGGAGGTCTG	TCTGATGCGC	ATCAGTTGTC	TCAAGCACTT	GCTGATTAAG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCATTCAAG	CAGGATAGC	CACCTCTAC	TGCTCTCTGT	TGCTGTCTGT	1520
1521	GTCCAGCGGA	TCAATGTGAG	GAGTGTGTCA	CCCTTCCCTG	TGAACCGCGG	CATGACCTGT	AAAGGATGAAT	1600
1601	ACAGCATCTG	ATCTCCGCGA	TGACCCGCGA	CAACGCAAA	ACCTCTGACA	ACAGCTGCGA	CAGAGACCTC	1680
1681	TTCTCGCAT	TGCTTCTGCA	TATACAATCT	CACTCACTCA	CTCAACAGT	GTGAGAAATG	CTGATTCGAG	1760
1761	ATACAGCATG	ATTCTGGGTA	CAGCTTCTCA	GAAAGGAATA	GTGAGCAAGG	CAATTCGCTG	GAAGACGACT	1840
1841	CAACATGOGA	AATCTCGGTA	TGCTGTGTGA	TAAACTTTAG	CGAGTCTGAG	TTAAGAGCCT	ACTGATGTTG	1920
1921	TTCTTAAAGG	CATCTCTCAT	GATGCTTTGT	TTACATATCT	GAACAAGGCT	TCAACATCTC	AACCTATGGA	2000
2001	ATTCTTGAAG	TCTGCTCTG	CGACTTCTG	TACATGGGGA	AGCATATCAT	AGCAGGAAGC	CAGGAGGGGT	2080
2081	AGTTTCAATG	CGAAAGTCTG	TTTCTCCGTT	TTTCTCCGTT	ACAGATATAG	GAATGATGCA	TGCCAGATGT	2160
2161	GGCAGCTTGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATAG	CCCTCTCTCT	CGAGATGTTT	TGCAACATCT	2240
2241	CGACCATATG	CTACTGAGGT	TTGCTGTGCA	GCTCTGACCA	GATGTCTACC	TGTTGTTTGT	TCAAAAAGCT	2320
2321	GGGCGACCAT	GGACATATCT	CTCTCATGAA	AAAAGTTTTT	TTATAGATT	CCCTCAACAT	TCTATGAAG	2400
2401	CGGCTTTAAA	AAATGTTTCT	ACTCTCTTAA	GGTCTTTAAT	ATCTCAAGCT	GAGCTCATCT	AGGACGGAGG	2480
2481	ATGTTGCGGT	CTCTGTGTTA	CGAGATCTTC	AAGTGCTGTA	AGAAGTCTCT	TTGTCGGGAC	GCTACGTGGA	2560
2561	GCTCTACTTC	CTGATAGGCA	ACACTTTGTA	TTTACATGGA	AGAAGTCTCT	CTGACGTGCT	TTTCTCATCT	2640
2641	CTGTACAGCA	GCTGTAGACA	GAGCTTTGTT	CGAGTCTGTA	CGACTTATG	AAAGAGATAC	GAAGGATGCT	2720
2721	GCAACAGATG	ACGGGCTTAT	TAGGACACAC	AGCTTCTCTT	GAGATGCTTC	TGAGCTATCA	GTACAGCCTC	2800
2801	AATGGCCACC	CGCCAGATGA	GAAGCAGTGA	GAAGCAGCCA	CATGGCCGAG	ATCCATGTCA	AAAATGGGGA	2880
2881	ATGCCAGCAC	CGCCGAGCTG	AGGAAGAGGT	GGCTGCAGAC	ATATATCTAC	ACGGAAGGCG	GTGTTTAGAC	2960
2961	CGGCATATGT	GCTATGTGCA	GCTAACAGCC	CTAGTGGCAG	TCCATGATGT	AGAAGCTGAG	GTGACGAGAT	3040
3041	CGCCTTCAAG	GTGATATACC	CAATATCTGA	CGAGGAGGCC	TGAGACTCTG	AAAGCCGAGG	GCTACGAGCT	3120
3121	ACGAGAGGTT	GCTATGGGAG	CTCTGTAGG	AGTGCACGGA	CTGATTTTGA	GTATCTGGA	TAAATTTGTT	3200
3201	ATTCTAACAAT	TTATATCCCT	CATTATTTAG	AAAGCGAGGG	CTCTCTAAAC	TTATCTGGA	TAAATTTGTT	3280
3281	GGAAACCAAA	CTCAACACCT	TGTGGAATAT	TTTCTCAGGA	TTCTGATTTCT	AAAGTATGCA	ACCATCAAGT	3360
3361	TCAAAATGAT	ACCAAGATCT	GGCAAGTCTA	ACCTTAAGGA	CTGAGTTTGA	GAGATCTCCAC	ACATATCCGC	3440
3441	ATCTCTCTCT	TTTGTGAGAA	AGAGTTGCAA	GAAAGGAGAA	GTGGAAGAGG	GTGCAAGAGC	GGGCACCAT	3520
3521	TGAGATGACA	TTTACGCAAG	CCGAGAGAGG	AGAGGGCCGG	GTACGAGCAC	CACATCTGAC	TGAACCCCAT	3600
3601	TACACTCTCT	CCCTTATGTT	AGAAGAGCGA	CTCTCTCTAT	GTGAGAGGCT	GGCCGAGGAT	GGCCGAGGAT	3680
3681	ATACCTGAGA	TGAGTAAAGA	GGTGCGGGAG	CTCCGCGCAG	CCACTAGCAT	ATGTCGGGAG	TTCTTTAGAT	3760
3761	CNAAGCTAGC	GGCAGGTGGA	GTGTTCAAGT	CAATGCTGGG	AGTTTCTCAG	CAATTGTGAG	AGCTTGGG	3840
3841	CAAGGCTATG	TCTTGACATAT	AAAGTGAAGC	TGCTTAAAGA	ATCAGAGAGA	CGAGCTCTCT	ACCATCAAGT	3920
3921	CGGCTAAGG	AACTTCTGAT	TAAAGAAGAC	CAGCTCGAGT	CGAGATGACC	CGAGATCTCT	CCGTTGTTGT	4000
4001	GAGGCTGCTT	CGAAATGCTG	ATGGCAGAGT	CTGCCCCCTG	TGAGATGACT	TCCAAGGCA	ACTACTGGG	4080
4081	TCAAGCCGCT	CAGTGGGACT	CCACAGCTC	CTCTCTAACT	CAACACATCT	CAAGCTGCTT	TTCTTTAGAT	4160
4161	ATGCCCCGTG	TGTTGGGACT	TCGTTTGCTA	TTTGCAGACT	CGAGATGACC	CGAGATCTCT	CCGTTGTTGT	4240
4241	CAGGAGGAGC	AGAGGGGAGG	GGGAGAGAGA	GGAATTAAGG	CAAGCTGCTT	TCCAAGGCA	ACTACTGGG	4320
4321	AGAAAGTGCA	CATATTTTTT	TTAATCTCAC	TGCAATATAT	CAAGCTGCTT	TTCTTTAGAT	TTCTTTAGAT	4400
4401	TTCTTGAGCT	GACTTAGATG	TATATTTCTC	TGTCAGAGTA	GGGAGGAGCT	TGCTGCTGAT	CTGTCGGGAA	4480
4481	ATGCTAATGA	CAGTAGAGGC	TGCACTGACA	TGATGCTGCT	TGTTTGAAGT	AGATGGCTTA	CAGAAAAAAA	4560
4561	ATTACAGCTG	CGAAATCTTC	TAGTTTGTTC	TAGGAGTATG	GGGAGGAGCT	TGCTGCTGAT	CTGTCGGGAA	4640
4641	ATAGAGGAGC	AATATGAGAG	TACTGAGCTC	AGACATCTCA	TGTTTGAAGT	AGATGGCTTA	CAGAAAAAAA	4720
4721	TCATGCACTC	CGGAGCGCTC	ATATATGTTT	TACATTTCTA	TTATTCGCTT	ACTGCTGCTG	GCTTATGATC	4800
4801	TGTGATATGT	TGTGCTGTGT	CCAGTATATG	CAATACACTT	TAATGGTGTG	TTTGTGCTAT	AAATATGTC	4880
4881	TGTATCAAGG	TCCTTACT						4960

Fig. 10A

	10	20	30	40	50	60	70	80	
1	MEGHVMIAPL	FTILNQLFRV	LTRATQEEVA	VNVTRVIMV	VAQCHEEGLE	SHLRSYKYVA	YKAEPPYVASE	YKIVHEELTK	80.
81	SMITILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAOHLIEN	SKVKLLRNQR	FPASYHUAEE	TVVNMMPHI	TQKFGDNPEA	160
161	SKUANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFETKFEF	LRVVCNHEHY	IPNLMPMPFG	KGRIGRYQDL	240
241	QLDYSLTDEF	CRNHFLVGLL	LAEVGTALQE	FREVRLIAIS	VLRNLLIKHS	FDDRYSRSH	QARIATLYLP	LPGLLIENVQ	320
321	RINVRDVSPF	PVNAGMTIVK	ESLALFAVNP	LVTPOKGSTL	DNSLHKDLIG	AISGIASPTT	TSTPNINSVR	NADSRGSLIS	400
401	TDSGNSLPER	NSEKSNLDR	HQSSTLGN	VVRCDKLDQS	EIKSLMCFPL	YILKMSDDA	LFTYNNAST	SELMOFFTIS	480
481	EYCLHOFQFM	GKXYIARQCE	GLGPTVDRK	SOTLPVSRRR	TQPMHARLQQ	LGSLNLSLTT	WHSYGHSDAD	VLAQSLLEAN	560
561	IATEVCLTAL	DTLSLFTLAF	KNQLADHCH	NPLMKRVFDV	YLCFLQHQGS	ETALQNVTTA	LRSLIYKFPS	TFYEGRADMC	640
641	AAICYEILKC	CNSKLSIIRT	EASQLLYFLA	RNNFDYTGKK	SPVRTLQVI	ISVSQLIADV	VGIGETRFQO	SLSIINNCAN	720
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWDSMARIH	VKQGLSEAA	800
801	MCYVHTALV	AEYLTRKGVF	ROGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880
881	KLIPIIYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISORLL	KLYSDKFGSE	NVKMIQDSGK	VNPEDLDSKY	AYIQVTHVIP	960
961	FFDEKELQER	KTEFERSHNI	RRPMFEMPFT	OTGKRQGGVE	EQCKRRTILT	AIHCFPPYVK	RIPVMYOHHT	DLNPPIEVAID	1040
1041	EMSKKVAELR	OLCSSAEVIM	IKLQKLQGS	VSVQVNAGPL	AYARAFLDLT	NTKRYPDNKK	KLLKEVFRQF	VEACQCALAV	1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLM	IFNAISGTTT	STWVHGWTSS	SSVV	1194
	10	20	30	40	50	60	70	80	

FIG. 10A (cont.)

	10	20	30	40	50	60	70	80
1	AATGTGAATA	CGACTCAGTA	TAGGGCGAAT	TGGGTACGGG	GGCCCGCCCT	GAGGTGGAGG	GTGTGATGTA	GCTTGTATTC
81	GAATTTGGCA	CGAGTTTTC	ACCATCAGCA	AAACCAGGAA	TTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCGAGCTG
161	ATGAAGAACA	CCCAAGTTGG	CTACATCTCT	CCATGTCGAG	CTGTGACAC	TCAGTTAAAT	GAGCAGCGAA	GAAGAGCGAT
241	GTGCTTGAAA	GGCAAGTTGG	CTACTCTGAG	CTTCCGCCCT	TGAAAGACGG	AGAGGTGGTG	ACAGCGGAGC	AGCCATATCC
321	GGGTCTGGCG	AACCTTCTCT	CGGCTATCT	CTTCCGCCCT	GAGCTTGGGA	TGGCGAGCGA	TTATGTTCCG	GAATTTAAAT
401	GGGTAGTAGT	AGGCAAGCCA	CTGCTGAAA	TTTCCACTCA	AGCTTTAGCA	AGCAAGCTTG	TCAGAGTACG	CATTACAGTA
481	ATTTTGTCCA	GTACTTGTAG	AAACAGCACT	CTGAGGCCCA	GGCTTTTCTT	ACAGAGTATC	TAAGAGTACT	TAAGAGTCTG
561	CATTCGATGG	AAGGCAAGCT	GATGATCGCC	TTCTTGCCCA	CTATCTGAAA	CCAGCTGTGA	TCAGAGTACG	CCAGAGCCAC
641	ACAGAGAGAA	GTGCGGGTGA	ACGTGACTCG	GOTCATTATT	CATGTGGTGT	CCAGCTGTGA	TGAGAGAGCT	TGAGAGAGCT
721	ATCTGTAGAG	ATATCTTAGA	TAGCTTACCA	AGGCTGAGCC	ATATGTTCGC	TGTGAATACA	AGACAGTACA	GAATTAAGAT
801	ACCAATATCA	TGACCAAGAT	CTTCCAGCTT	CTGCGGATTT	TGCTCACCAG	CAACAAGATA	CTGAGGTACT	CATGTGTTCT
881	CTTTGATGTA	CTGATCAAT	CTATGCGTCA	GCTATTGATA	GGCAACTCCA	AGTTTAAAT	GCTCGGAAAC	CAGAGATTTT
961	GTGCATCTTA	TCATCATGCA	CGCGAAACCC	TTGTAATAT	TCAGATGCGA	CACATCACTC	AGAAAGTTGG	AGATAATCCA
1041	GAGGCACTTA	AGAAAGCGAA	TCATAGCCCT	GCTGTCTTGA	TCAGAGTACA	TTTCACTTTC	ATGAGAGGTT	GCTTGTGCTT
1121	CAAGCAGATC	AACAAGTACA	TGATGTTTTT	TGCTCTTGGA	GACCCAAGGA	CCCTTTTGGA	ATGAGAGGTT	GAATTTCTCC
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTT	GTTTGAACCT	ACCAATGCGA	TTTGAANAAG	CTGTACTAGA	TAAGATACAA
1281	GACTCTCGAG	TTGATCTGAT	ATTACAGATG	GAGTTTCTGA	GAAACCACTT	CTTGTGGGGA	CTGTACTAGA	GTGAGGTGTT
1361	GACAGCCCTC	CAGAGTTTCC	GGGAGGTGCT	TTTGATGGCC	ATCAGTGTGT	TCAGAAAGAT	GCTGATAAAG	CATTCTTTTG
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAAG	CAGAGTATAG	CAACCTCTAC	CTGAGCTGTG	TTGTCTGCTG	GATTGAAATC
1521	GTCACAGCGA	TCATGTGTAG	TAGATGTGTA	CCCTTCTCTG	AGCCCTGGGA	CATGAGCGTG	AAGATTAAT	CTCTGGCTCT
1601	ACACGCTGTG	AATCTCGGTT	TGACGCGCGA	GAAAGGAAAG	ACCTCTGGGA	AGAGCTCTGA	CAGAGTACTG	CCGCGGCCCA
1681	TTCTTCCGAT	TGCTTCTTCA	TATGAACCTT	CAACTCCAAA	CATTCAACAT	GTGAGAGATG	CAATTCCTCT	AGAGTCTCTC
1761	ATAGCAGAGT	TTGCTGTGAA	CAGCTCTTGA	GAAAGGAATA	GTGAGAGAGT	CAATTCCTCT	GATAGAGCAT	TTGAGTCTCT
1841	CACATTTGGA	TTGCTGTGAA	TGCTGTGTA	TAAACTTTGAC	CAGTCTGAGA	TTGAGTCTCT	CTGATGATCT	TTCTCTTCTC
1921	TTCTAAGAGT	CATGCTTGAT	GCTGCTTTG	TATCATTTTG	GAACAAGGCT	TCATCATCTG	AACCTATGGA	TTTTTTTACA
2001	ATATCTGAAG	TGCTGCTGCA	CCAGTTTCCG	TACATGGGGA	AGCAAGTACT	AGCAAGGAGC	CAGAGAGGTT	TGGGAGCCAT
2081	ATTTCTGAAT	CGAAAGTCTG	AGACATTTCT	TGTTTTCCGT	CCACTCTGAG	GCGATGTTCT	GCGTTTAAAG	CATTCTTTTG
2161	CGACGCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CGCTTCTTCT	ATTTATCTTT	TCCTTAAATC	GAATTCATCT
2241	GCACACATG	CTACTGAGGT	TTGCTGTGAA	GCTCTGGACA	GATCTCTTAC	TTGTTTCTT	TCCTTAAATC	CAGTCTGAAA
2321	GGCCGACAT	GGACATAATC	ACTCGCTTAA	AGAGTCTTCT	ACTCAAGCTT	TTGTTTCTT	TCCTTAAATC	GATTCGAGAT
2401	CGGCTTTAAA	AAATGCTCTC	ACTCGCTTAA	AGAGTCTTCT	ACTCAAGCTT	TTGTTTCTT	TCCTTAAATC	GATTCGAGAT
2481	ATGTTGTGCG	CTGTTGTGTA	CGAGATTTCT	AGTGTCTGTA	AGATCAAGCT	GAGTCTCTCT	AGAGTCTGAG	CTTCCAGCTT
2561	GCTCTACTCT	CTGATGAGGA	ACAATTTTGA	TTACACTGGA	AGACAGATCT	TCCTTCTGCA	AGATTTTGA	CTTCCAGCTT
2641	CTCTGACGCA	GCTGTATAGCA	CAGCTTTTGA	CGATTGGGGA	AGACAGATCT	TCCTTCTGCA	AGATTTTGA	CTTCCAGCTT
2721	GCACACAGTG	ACCGCTCTCT	TAAAGCACAC	AGCTTCTCTT	CGATGCTGGA	GGATCTTAC	AAAGAGGATC	CTTCCAGCTT
2801	ATGCGCAGCC	CGCCGAGTCA	AGAGAGAGCT	GCTCTGGGGA	GAGATGCTG	TGGAGCTGGA	GAAGAGGATC	CTTCCAGCTT
2881	ATCGCAGCAT	CGCCGAGTCA	AGAGAGAGCT	GCTCTGGGGA	GAGATGCTG	TGGAGCTGGA	GAAGAGGATC	CTTCCAGCTT
2961	GAGCAGATGT	GCTATGTGCA	CTACACAGCC	CTAGTGGGGA	CATGCGCAGC	ATCATGCTGA	AAATGGGGA	TCTCTGAGAG
3041	CGCTTCTGAG	GCTATTACCC	CAATCAAGCT	CGAGGAGGCC	CGATGCGCAG	ATCATGCTGA	AAATGGGGA	TCTCTGAGAG
3121	ACGAGGATGT	CTGCTTGGAG	CTCTCTGAGC	AGTGGCGAGA	CGATGCGCAG	ATCATGCTGA	AAATGGGGA	TCTCTGAGAG
3201	ATCTCAAGAC	TTATCATCTC	CTGCTTGGAG	AGTGGCGAGA	CGATGCGCAG	ATCATGCTGA	AAATGGGGA	TCTCTGAGAG
3281	GCACACCGAA	CTACACCGCT	TTGCTGAAAT	TTCTGAGGGA	ATTTCTTTGA	AGATGAGGAT	GAAGAGGATG	ATATTTTACA
3361	TCAAATATGT	ACAGAGTCTC	GGCAGGTCTG	AGCCTTAGGA	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
3441	ATCCCTCTCT	TGAGTGAJAA	AGAGTTGCGA	GAAAGGAGAA	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
3521	TGAGATGCGA	TTTATGCGGA	CGGAGGAGAG	CGAGGCGGGG	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
3601	TACAGTCTCT	CTCTTATGTA	AGAGTGGGGA	CTCTCTTAA	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
3681	ATTCAGCGGA	TGATGTAAGA	GGTGGCGGAG	CAATGCTGCG	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
3761	CAACTCTCAG	GGCAGCGGTA	CTCTCTTAA	CTCTCTTAA	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
3841	AGACAGGATA	CTCTGAGCAT	AAATGAGGAT	CAGCTGAGAT	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
3921	GGGTAAAGAG	AACTCTGATG	TAAAGAGGAT	CAGCTGAGAT	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4001	GGAATCTTCT	GAAATCATGC	TAGAGGAGAT	GCTGCCCTGT	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4081	TCAGGCCCAT	CAGTGGGACT	CCACAGAGCA	CAATGCTTCA	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4161	ATGCGGCTCT	TGCTGGGACT	CTCTTGTGCA	GGATGATTTT	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4241	CGAGGAGGAC	CTCTGGGACT	GGGAGGAGTA	GGATGATTTT	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4321	AGAGAGTGCA	CATATTTTCT	TAAATTTCTC	TTGCGAGATG	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4401	CTTGTGAGTG	CGCTTAGATT	TTGCTTCTCT	TTGCGAGATG	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4481	ATCTACATGT	CGAGGAGGCG	TGCACTGAGCA	TTGATGCTCT	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4561	AATCAGGAGTG	CGAAATCATG	TAGTGTGTT	TAGAGGATG	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4641	ATGAGGAGAG	AATGATGAGC	TAGTGTGTT	TAGAGGATG	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4721	TCATGAGCTC	CGAGGAGTCT	ATATATGAT	TACATTTCTA	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4801	TGTATGATAT	CTAGGCTGAT	CCAGTATATG	CAATACACTT	CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG
4881	TGTATGATAT	CTTCTACT			CTCTCTTAA	TGATCTGGA	TAAATTTGGT	TCGTAAGATG

FIG. 10B



	10	20	30	40	50	60	70	80
1	MEGHVMIAPL	PTILNQLFRV	LTRATQEEVA	VNVTREVIIHV	VAQCHEEGLE	SHLRSTYKTA	YKAEFYVASE	YKTVHEELTK 80
81	SMITILKPSA	DPLTSNKLRL	YSMFFFDVLI	KSMAGHLIEN	SKVKLLRNQR	FPASTYRAAE	TVVNNLMPHI	TQKFGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPILNLPMPFG	KGRIGRYQDL 240
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTLAQE	FREVRLIAIS	VLRNLIKHS	FDDRYASRSH	QARLATLYLP	LPGLLIENVQ 320
321	KINVRDVSFF	PVNAGMTVKD	ESLALPAVNR	LVTPQMSLT	DNSLKHDLIG	AISGLASPTT	TSTPWINSVR	NADSRGSLIS 400
401	TDSGNSLPER	NSEKSNSLDK	HQOSSTLGSN	LVTPQMSLT	EIKSLIMCFL	YILKMSDDA	LFTYMNKAST	SELMOFFTIS 480
481	EVCILHOFYM	GKRYIARNOE	GLGPTVHDK	VVRCDLQDS	TQMMHARLQ	LGSLDNLSTF	NHSYGHSDAD	VLHQSILLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KQQLLADHGH	NPLMKKVFDD	YLCFLQKHQS	ETALGNVFTA	LRSLIYKFPS	TYFEGRADMC 640
641	AALCYEILKC	CNSKLSSEIT	EASQLLYFLM	RNNFDYTKKK	SVFRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSTINNCAN 720
721	SDRLIKHTSF	SSIVKDLTKR	IKTVLMATAQ	MKEHENDPEM	LVLDQYSLAK	SYASTPELRK	TNLDSEMARIN	VYKGLSEAA 800
801	MCYVHVITALV	AEYLTRKGVF	RQCTAFRVI	TPNIDEASM	MEDVGMQDVH	FNEQVLMELL	EQCADGLWKA	KRYELIADIY 880
881	KLIIPITYEKR	RDFEFEDGK	EYTYKEPKLT	PLSEISORLL	KLYSDKFGSE	NVRMIQDSGK	VNPKDLSKY	AYIQVTHVIP 960
961	FFDEKELQER	KTEFESHGNI	RKPMFEMPT	QTGKRGQVE	EQCKRKILT	AIHKFTYVVK	RIPVMYQHT	DLNPIEVAID 1040
1041	EMSKVYAELE	QLCSEAEDVM	IKLQLKQGS	VSQVNRAGPL	AYARFLDDT	NTRKYFDNKV	KLLKEVFQF	VEACGQALAV 1120
1121	NERLIKEDQL	EYQEEKANY	RENAKELSEI	MHEQICPLEE	KTSVLNLSH	IFNAISGTP	STMVHGTSS	SSVV 1194
	10	20	30	40	50	60	70	80

FIG. 10B (cont.)

	10	20	30	40	50	60	70	80
1	AAITUTAAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCTCCCTCT	GAGGTGAGG	GTATCGATAA	GCTTGATATC
2	GAATTCGGG	GAGGTTTTAC	ACCATTACCA	AAACCCAGAA	TTTTATGATG	GAGTAAATAT	AGAGTTGGCC	ACTCAGCTGC
3	ATGAAAGAGT	CGACTGCTAT	CTCAGCATTC	TCGATGTGCA	CTGTGACAAC	TCGAATTAAT	ACAGAGTCGA	GAGAGAGGAT
4	CTCGTTGAATA	CCCACTGCTT	CTTCCCTCTC	CTTCCCTCTC	TGAAAGACGG	AGAGGTGGTG	ACAGCGGAGC	AGCAATATCC
5	GGTCTGGGG	AGACTTCTCT	CGGGCTATCT	TTCGTACCAA	GAGCTTGGGA	TGGCGAGGCA	TATGTGTCCG	GAAATATATC
6	GGGTAGATGT	AGGCGAAGCA	CTTCTGAAAT	TTGCTACCTA	TCGTGTTTCT	ACAGGGATAT	TCAGAGTATC	CATTATTAAT
7	ATTTTTTCCA	GTACTCTCAG	AAGAACGGAAT	CTGAGGCCCA	AGCCTTAGGA	AACGAAGTCT	TAAAGTACCT	TAAAGTATAT
8	CATCGGATGT	AAGGCGAGCT	GATGATGGCC	TTCTTGCCCA	CTACTCTGAA	CCAGCTGTCT	CGAGTCTCTA	CAGAGGCCAC
9	ACAGGAGAGA	GTGCGCGGTA	ACGTGACTCG	GGTCATTATT	CATGTGTGTA	CCGATGTGCA	AGAGCTGCTA	TGAAGAGGCC
10	ACTTGAGTGT	ATATGTATAG	TACGGCTGTA	AGGCTGAGCC	ATATGTGTCT	CCGATGTGCA	TGAGGAAAGG	TTGAGAGGCC
11	ACCAAACTCA	TCGACACGCT	CTTCCAGGCT	TTCTGAGGCT	TCCTCACCAG	CAACAACTCA	CTGAGCTACT	CATGTTTCTC
12	CTTTGATGTA	CTGATCAAA	CGGTAAGCTA	GCATTGATAT	GAGAACTCCA	AGATTAAGTT	CTGCGAAGC	CATGTTTCTC
13	CTGCATCTTA	CTCATATGCA	GGGGAAGCC	CTGTCTCTCA	CTGATGCTCA	CAACTCACTC	AGAGTTTCTG	AGATTAATCA
14	GAGGCATCTA	AGAAAGCGAA	TGACAGCTT	TCGCTCTTGA	TCAGAGATGT	TTTCACTCTC	ATGCGACGGG	GCTTTGTCTT
15	CAAGCAGATG	AACCACTACA	TTAGCTTTT	TGCTCTCTGA	GACCCCAAGA	CCCTCTTCTG	ATGAGTATCA	GAATTTCTCT
16	CTTTAGTGTG	CAACATAGAA	GATTAATATC	COTTTGAATT	ACCAATGCTA	CTGTGTGCTG	CGAGATATCA	AGATTAATCA
17	GACCTTCAGC	CTGACTACTC	ATTAAACAGT	GAGTTCTGCA	GAACCAACTT	TTTGGAAAGG	CGAGATATCA	AGATTAATCA
18	GACAGCCCTC	CAGAGATTCCT	GGGAGGTCTG	TCGATGTGCT	ATCAGTGTGC	TCAGAGACTC	CTGTTACTGA	GCGAGGTGCT
19	ATGACGATGA	TGCTTCAAGG	AGCCATCAGG	CAMGATAGCT	CACCTCTCAC	CTGCTCTCTG	TTGTTTGTCT	GACTTTCTTT
20	CCAGCTCGGA	TCAGATGTAG	GAGTGTGTGT	CAAGGATAGC	TGAAAGCGGG	CGAGCTGTCT	AGAGTATGAT	CCCTGCTCTC
21	ACCACTGTGT	AATCGCTGTG	TGAGCGCGCA	GAGGAGGAGC	CTGCTCTGCA	ACAGGCTGCA	CAGAGCTGCA	CTGGGGCGCC
22	TTCTCCGGAG	TGCTTCTTCA	TATACAACCT	CAACTCCAAA	CTGCTCTGCA	ACAGGCTGCA	CAGAGCTGCA	AGAGTATGAT
23	ATAAACAGAG	ATTCTGGGTA	CAGGCTTCCA	GAGGAGATA	CTGAGAGAGG	CTGAGAGAGG	CTGAGAGAGG	AGAGTATGAT
24	CACATTTGGA	AACTCCGCTG	CTGCTGTGTA	TAACTTTGAC	CTGAGAGAGG	CTGAGAGAGG	CTGAGAGAGG	AGAGTATGAT
25	CTTTAAAGAG	CATGCTGTAT	GTCTCATATT	TACATATTGT	CAGTCTTGGA	TAAAGAGGCT	CTGAGAGAGG	AGAGTATGAT
26	ATATCTGAAG	TTGCTGTGCA	CCAGTTGGCT	TACGCTGGGA	GAACAGACTG	TAAAGAGGCT	CTGAGAGAGG	AGAGTATGAT
27	AGTTCTGATG	CGAAGTCTCT	AGACATCTGC	TGTTTCTCTT	AGGCGATACAT	AGGCGAGGAC	CAGGAGGGGT	CTGAGAGAGG
28	GCAGCTGTGA	CTACTCTGCT	ACTTTTAAAG	CAAGCTATGC	AACGAGAACG	GAATGTGCTG	TCGAGAGAGG	CAGAGCTGCT
29	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CCACTGTGAC	CGAGATGTCT	TGCTGAGAGG	CTGAGAGAGG
30	GGCGGACAT	CAGCATATCT	ACTGCTCTTA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
31	CTTTTCTTAA	AAATGCTGTA	ACTGCTCTTA	AGTCTCTGTA	GATGTCTTAC	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
32	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	TTATAGTCTT	CCCTCAACAT	TCGATGAGG	CTGAGAGAGG
33	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
34	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
35	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
36	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
37	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
38	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
39	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
40	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
41	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
42	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
43	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
44	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
45	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
46	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
47	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
48	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
49	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
50	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
51	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
52	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
53	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
54	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
55	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
56	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
57	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
58	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
59	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
60	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
61	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
62	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
63	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
64	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
65	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
66	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
67	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
68	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
69	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
70	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
71	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
72	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
73	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
74	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
75	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
76	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
77	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
78	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
79	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
80	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
81	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
82	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
83	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
84	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
85	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
86	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
87	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
88	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
89	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
90	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
91	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
92	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
93	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
94	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
95	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
96	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
97	ATGTTTCTG	CTGATGAGGA	CAACTTTTGA	TTACATCTGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
98	CTTCTGAGCA	CGCTGATGCA	GAGCTTGTGT	CGATTTGGGA	ACTTCAAGCT	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG
99	GCACACATTS	CTACTCTGCT	CTCTCATGAA	AGTCTCTGTA	CGCTTTCTCT	TTGTTTCTCT	TCGAGAGAGG	CTGAGAGAGG
100	ATGTTTCTG	CTGCTGTGTA	CGAGTCTTCA	AGTCTCTTAA	GATGTCTTAC	GAATGTGCTG	TCGATGAGG	CTGAGAGAGG

Fig. 10C

	10	20	30	40	50	60	70	80	
MEGIVMIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVLIHV	VACCKEKGLE	SHLSRYVYKA	YKAEPYVASE	YKTVHEELTK	80	
SMITILKPSA	DFLTSNKLLR	YSMFFFDVLI	KMAQGLIEN	SKVOLLKWR	FPASYSBAAE	TVVNMMPRI	TOKFGUNPEA	160	
SQWANHSLAV	FIKRCFTFMD	RGFVFKQIRN	YISCFAPGDP	KTLFEYKFEF	LRVVCORUEY	IPLKLMPFPG	KGRICRYQDL	240	
QLDYSLATDEF	CRNHFLVGLL	LREVGTLQGE	FREVLIAIS	VLSQKLLKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVQ	320	
RINVRDVSFF	PVNAGTIVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLIG	AISGLASPTT	TSTPHINSVR	NADSRGSLIS	400	
TDGNSLPER	NSEKSNLDDK	NOQSSTLGNS	VVRCKLDQS	EIKSLIMCFL	YILKMSDDA	LFTYMNKAST	SELMGFFTIS	480	
EVCLHQFOYM	GKRYIARNOE	GLGPVHERK	SQTLFVSRNR	TOMQJALQQ	LGLSLNSLTF	NHSYGHSDAD	VLAQSLKAN	560	
IATEVCLTAL	DTLSLTLAF	KNOLLADHGH	NPLAKKVFDP	YLCTLOKHQS	ETALKNVFTA	LRSLITYKPS	TTYEGRADMC	640	
AALCYEILKC	CNSKLSIRT	EASOLLYFLM	RNNFDYTGKK	SFVTHLQVI	ISVSOLLADV	VGLDSTFPOQ	SLSIINNCAN	720	
1 SERLLIGHTSF	SSDVKLITKR	IRTVMATAQ	MKEHNDPEN	LVDLQYSLAK	SYASTPELRK	TWLDSDARH	VKGDLSEAA	800	
1 MCTVHYTALV	AEYLTRKGVF	ROGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEVDLMEL	EOCADGLMKA	ERYELLADIY	880	
1 KLIIPYIKER	RDFFEDEDGK	EYTYKEPKLT	PLSEISORLL	KLYSDAPSE	NVPMIQDSGK	VNPKDLDSKY	AYIQVTHVIP	960	
1 FYDEKELQER	KTEFERSHNI	RRPFEMFFT	QJGRQOOVE	EOCKRTILT	AINCHPTVYK	RIPVHYOHT	DLNPTEVAID	1040	
1 EMSKQVAKLR	QLCSSAEVIDM	IKLQKLGLOS	VSVQVWAGPL	AYARAFLDUT	NTRYKPDNKK	KILKEVFROT	VEACQCALAV	1120	
1 NERLIKEDQL	EYQEDQKANY	RENACEISEI	MHEQICPLES	KTSVLPHSLH	IFNAISGTPT	STMVHGNTSS	SSVV	1194	
	10	20	30	40	50	60	70	80	

Flg. 10C (cont.)

	10	20	30	40	50	60	70	80
1	AATTTGTAATA	CGACTCTACTA	TAGGGCGCAAT	TGGGTACGGG	GGCCGCCCTC	GAGGTCCAGG	GTATCGATTA	GCTTGTATTA
2	GAATTTGACGA	CGAGTTTCTTA	ACCATCAACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGCTTGGCC	ACTCTAGCTCG
3	ATGAAAGAGCA	CCAGCTTTGTG	CTCACATCTCT	TCCATGTTCAG	CTGTGACACAC	TCAGTAAATG	GAGACAGAA	GAGAGAGGAT
4	CTGCTTTGAGG	CGAGTTTCTCT	CTTCCCTCTCG	CTTCCCTCTCG	TGAAAGAGCG	AGAGGTGGTG	ACAAGCGAGC	AGCAATGCCC
5	GGGTATGCGCG	AGGCGAAGCCA	CTGCTTAATA	TGGCTACCCA	GAGCTTGGGA	TGGCGACGCA	TTATGTGCTCG	GAATTAATAT
6	ATTTTITTTCCA	GTACTGTTCAG	AAACCGCAAT	CTGGAGGCA	CTGCTTTCTT	ACAGAGATAC	TCAGGATGTG	TTATTCACATA
7	CATCGCGATGG	AAAGCGACGCT	GATGATGCGC	TTCTTGCCCA	AGCTTTAGGA	AACGACCTTC	TAAAGTCTCT	TAAAGTCTCT
8	ACAGGAAGAA	TGTGGGTTTA	ACGTGATGCT	GCTTATAT	ATCTCTTAA	CGAGCTTTTC	CGAGTCTCA	CCGAGCCAC
9	ACTTGAAGGCT	ATATGTATTA	TACGGGTATA	AGGCTGAGCC	ATATGTGCTC	CCGAGTCTCA	TGAGGAGGGA	TGGAGAGGCT
10	ACCAATATCTA	TCAGATCAAT	CTTCTGAGCT	CTGCGGATTT	TGCTGATGAC	TCGTAATGCA	AGACATCTCA	TGAGAAAGCT
11	CTTGTATGTA	CTGATCAATG	GGGAAATCTA	CGATTGTGTA	TGCTGATGAC	CAACAAATCT	CTGAGTAACT	CATGTTTTTT
12	CTGCACTCTTA	TCATCATGCA	GGGAAATCTA	CGATTGTGTA	GAGAATCTCA	AGGTTAACTT	GCTGCGAAC	CAGATTTTCT
13	GAGGACTATTA	AGAAAGGGA	TTATAGCTTT	TTTAAATAT	GCTGATCTCA	CACATCACTG	AGAGTTTGT	AGTAAATAT
14	CAAGCAGATCT	AAACAATCTA	TGACTGTTT	TGCTCTGGA	TCAGAGAGAT	TTTTCACTTT	ATGACAGGG	GCTTTGTCTT
15	GCTGTAGTGT	CAACATGAA	CATTATATCT	CGTTGAACCT	ACCAATGGA	TTTTGGAAG	CGAGATTTCA	GAATTTCTCC
16	GAGCTCGAGC	TTGACTACTCT	GGGAAATCTA	GAGTGTGCA	GAUACCACT	CTGTTGGA	CGAGATTTCA	AGATTAACAA
17	GACGCGGCT	CGAGTCTGAG	AGGAAATCTA	TGCTGATGCT	ATCAGTGTG	TCAGAAAGCT	CTGATTAAG	GGAGAGAGCT
18	ATGACAGATA	TGCTGTAGG	GGAGTGTG	CAGGATGAGC	CACCTCTAC	CTGCTCTCT	TGCTGTCTCT	CATTTCTTTG
19	ATGAGCGGGA	TAAGTGTGAG	GGAGTGTG	CAGGATGAGC	TGAAACGCG	CATGACGCT	AGAGTAAAT	CCCTGCTCTT
20	ACAGCTGTG	ATGCTGCTG	TGAGCGCGA	GAGGAGGAGC	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
21	TCCTGCGCAT	TGCTTCTTCA	TACATAAGCT	CACCTCAAA	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
22	ATGAGCGGGA	ATTTGGGTGA	CAGCTTTCA	GAGGAGTAA	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
23	CTTTAAAGAG	CTGCTGCTG	CGAGTGTG	TACATATTT	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
24	ATCTTCTGAG	CGAGTGTG	CGAGTGTG	TACATATTT	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
25	AGTTCTATGAT	CGAGTGTG	CGAGTGTG	TACATATTT	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
26	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
27	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
28	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
29	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
30	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
31	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
32	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
33	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
34	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
35	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
36	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
37	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
38	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
39	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
40	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
41	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
42	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
43	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
44	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
45	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
46	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
47	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
48	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
49	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
50	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
51	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
52	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
53	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
54	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
55	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
56	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
57	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
58	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
59	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
60	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
61	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
62	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
63	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
64	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
65	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
66	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
67	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
68	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
69	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
70	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
71	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
72	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
73	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
74	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
75	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
76	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
77	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
78	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
79	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT
80	GGCAACATGT	CTACTGAGCT	TGCTGCTG	CGAGTGTG	CTGCTCTCT	ATGCTGCTG	AGAGTAAAT	CCCTGCTCTT

	10	20	30	40	50	60	70	80
MEGHVMAI	FL	PTILNOLFRV	LIRATQEEVA	VWTVRVIIHV	VAQCCEEGLE	SHLSSTVYKA	YKAEFVASE	YKTVHEELTK 80
SMITILKPSA	DFLTENKLLR	YSMFFFDVLI	KSMAGHLIEN	SKVKLLANQR	FRSYDHAAE	TVVRMLMPHI	TQKPGDNPEA	160
SKGANHSLAV	FKRRCFTFMD	RGVFVKQDNN	YISCFAPGDP	KTLFETVFEF	LRVYORREBY	IPLNLPMPFG	KGRIGRYOOL	240
QLDYSLTDEF	CRNHFLVGLL	LREVTGALQE	PREVKLIAIS	VJKNLLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVO	320
RINVRVSPFF	PVNAGMTVQD	ESLALPAVNE	LVTPOKGSIL	DNSLAKDLIG	AISGLASPTT	TSTPWINSVR	NADSRGSLIS	400
TDSGNSLPER	NSEKSNLQK	HQOSSTLQNS	VVKCRLDQS	EIKSLJACFL	YILKMSMDDA	LFTYMNKAST	SELMDFFTIS	480
EVLNHOFOYM	GKRYLAUNOE	GLGPTVHQRK	SUTLPSVRRR	TGQGHARLQO	LGSLSNLSIT	NHSYGHSDAD	VLRQELLEAN	560
LATEVCLTAL	DTLSLFTLAF	KNQLLADIGH	RPLMKKVFIV	YLCFLQRIQS	ETALONVFTA	LRLSLIYKPS	TTTGRADNC	640
AALCYEILKC	CNSKSSIRT	EASQLLYFLM	RNFDTYTKK	SFVRTHLQVI	ISVSQLIADV	VGIETRFQOQ	SLSIINRCAN	720
SDRLIGHTSF	SSDVKDLTKR	ROOCTAFKVI	TPNIDEASAM	LVDLQYSLAK	SYASTPELAK	TWLESMARIN	VKGDLSEAA	800
MCYVHVITAL	AEYLTKRGVF	ROOCTAFKVI	PLSEISORLL	MEUVGQDVH	FNEDVLMEIL	EQCADGLMKA	ERYELLADIY	880
KLIIPIYEKR	RDFFEDSKK	EYTYKEPKLT	QTKRQGGVE	KLYSDKFGSE	NVNMIGDSKG	VNPKDLDSKY	AYIQVTHVIP	960
FFDEKELOER	KTEFERSHNI	RNFDMFPT	QTKRQGGVE	EQCKRTILT	ALHCFYTVK	KIPVWYQHRT	DLNPIEVAID	1040
EMSKVAELR	QLCASSAEVM	IKLQKLQSS	VSVQVHAGFL	AYARAFLODT	NTRKYDUNKV	KLLKVFVRQP	VEACQALAV	1120
NERLIKEDGL	EYOEEMUANY	REMAKELSEI	MDEQICPLES	KTSVLPHSLH	IFNAISGTTT	STMVHGMTSS	SSVV	1194
	10	20	30	40	50	60	70	80

FIG. 10D(cont.)

	10	20	30	40	50	60	70	80
1	ATTGTAAAT	CGACTCACTA	TAGGCGGAAT	TGGTACTGG	GGCGGCCCC	GAGGTGTGAG	GTATCATGATA	GCTTGATATC
2	AATTTCGCA	CGAGTTTTAC	ACCATCACCA	AAACCCGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC
3	TGAAAGACA	CCACCTGTGT	CTCATCTTCT	TCCATTTGAG	CTTTTGACAC	TCAGTAAAG	GAAGCACGAA	GAAGAGGGAT
4	TGCTTGAAT	CCCAAGTTGG	CTTACTCTGG	CTTCCCTCTC	AGAGGTTGTT	ACAGGCGGAG	AGCAGATCCC	320
5	TGCTTGGCG	AACCTTCTCT	CGGCTATCTT	TGGCTACCAA	GAGCTTGGGA	ACAGGAGTAC	TTATGTTTCT	GAATTTAAAT
6	TGTTAGATG	AGGCAAGCCA	CTTGTGAATA	TTTCACTCA	CTTGTGTTCT	ACAGCTTTTC	CGAGTCTCTA	TAGAGTTATC
7	TTTTTTCCA	GTACTTTGAG	AAACACCGAT	CTGAGGCCCA	AGGCTTTAGGA	AACGAACTTC	CGAGTCTCTA	560
8	ATGTCATAT	AAGGCGAGT	AGTGTGTGCC	TTCTTGCCCA	CTATCCTTAA	CCAGCTTTTC	CGAGTCTCTA	560
9	ACAGGAAGA	CTGCGGCTGT	TAGCGTATPA	CTTCCGATTT	CATGTGTGTT	CCGAGTGCCA	TGAGGAAGGA	CGAGGCCAC
10	ACTTGAAGTC	ATAGTTTAA	TTCTCAAGCT	GGTCTATATT	ATATGTTGCC	TTCTGAATTA	GAAGCATGTA	TGAAAGACTG
11	ACCAATATCA	TGACCCAGAT	CTGAGGCTCA	GGTCTGAGCT	TCCCTCACCG	CAACAACTTA	CTGAGTACT	CATGTTTATT
12	CTTTGATGTA	CTATCATGCA	CGAGGAACCG	TTGTAATTA	GAGAATTCOA	AAATTTAGTT	GCTGCGAATC	CAGAGATTTC
13	TGCGATCTTA	AGAAAGCGGA	CTATAGGCTT	GGTCTCTGGA	GGCTTCTGGA	CAACATCTTC	AGAAATTTGG	AGATATTCOA
14	CAGGCAAGTC	AACAACATCA	TTAGCTTTTT	TGCTCTCTGA	GACCCATGTA	TTTCACTCTT	ATGAGCAATG	GCTTGTCTCT
15	GTGTAGTTGT	TAACCATGAT	CATTATATTT	GGTTGAACAT	ACCAATGCOA	CCCTCTTTTA	ATACAAATTT	GAATTTCTCC
16	GACCTCAAG	CTGACTACTC	ATTATACAGT	GAGTCTGCA	TGCTGTGCA	GGCTCTTTTA	AGATTAATCA	1280
17	GACGAGCTC	CAGGAGTTCT	AGGAGGTTCT	TTCTCTCTT	TCATGATGCC	TCGAGAGAG	AGCAGATGTA	GGAGGTTGGG
18	ATGACAGATA	TCTTTCAGGG	AGGCACTAGG	CAGGATAGC	CACCTCTCTC	CAACGCTTCA	CAGGATAGT	CGAGGTTGGG
19	GTCAGCGGA	TCATATGAGT	GGATTTGTTT	GGAGGATGCA	ACCTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
20	ACCAAGTTGT	AATCCGCTGG	TGAGGCCCA	GAAGGATTA	ACCTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
21	TTCTCGGAT	TTCTTCTCCA	TATACAACTT	CACTCTCAAA	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
22	ATAGAGCAG	ATTGCGGTAA	CAGCTCTTCA	GAAGGATTA	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
23	CAGATTTGGA	AATTCGTTGT	TGCTGTTGTA	TAACTTTGAC	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
24	CTTTTAAAG	CTGATCTGAT	GATGCTTTT	TTACATATTG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
25	ATATTCAGG	TCGCTCTGCA	AGCATCTTGA	TGTTTCTGCT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
26	AGTTTATGAT	CGAAATCTG	ACTTTTAAAC	ACTGCTGACA	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
27	CGAGCTTGA	TACTCTCTCT	ACTTTTAAAC	ACTGCTGACA	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
28	GGCAACATT	CTACTGAGGT	TTGCTGTGCA	GGTCTTTAAT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
29	GGCGGCCAT	GGACATTAAT	CTCTCATGAT	AAAGTTTCTT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
30	CGGCTTTAAA	AAATGTTCTT	ACTGCTTTAA	GGTCTTTAAT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
31	ATGTTGCGG	CTCTTTGTTA	CGAGTTCTCT	AAATGTTCTT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
32	GGCTTACTCT	GGTATGAGGA	AGCATCTTGA	CTGATTTGTT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
33	CTGTGAGCA	GGTATGAGGA	AGCATCTTGA	CTGATTTGTT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
34	GGCAAGGAT	ACCGGCTTAT	TAGGCAACAC	AGCTTCTCTT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
35	AATGCGCAC	GGCCAGATGA	AGAGGATGTA	GGTCTTTAAT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
36	ATGCGAGCAG	GGCCAGGCTG	AGGAGGATG	GGTCTTTAAT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
37	GGAGCATATG	GCTATGTTCA	GGTCTTTAAT	GGTCTTTAAT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
38	CGCTCTCAG	GCTATGTTCA	GGTCTTTAAT	GGTCTTTAAT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
39	ACGAGATATG	GCTATGTTCA	GGTCTTTAAT	GGTCTTTAAT	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
40	ATCTCAGAA	TTATCATCCC	CATTATTGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
41	GGAAACCAA	CTCACACGCG	TGTTGGAAT	TTCTGAGGGA	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
42	TCAAAATGAT	ACAGGATGAT	GGCAAGTGA	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
43	ATCTCTCTCT	TTTGGAAGAA	AGAGTTGGA	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
44	TGAGATGCA	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
45	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
46	TGAGATGCA	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
47	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
48	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
49	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
50	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
51	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
52	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
53	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
54	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
55	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
56	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
57	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
58	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
59	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
60	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
61	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
62	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
63	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
64	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
65	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
66	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
67	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
68	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
69	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
70	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
71	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
72	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
73	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
74	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
75	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
76	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
77	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
78	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
79	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT
80	ATCTCTCTCT	TTTGAGGAGA	AGAGGAGAG	AGTTCGAGG	CACTCTGACA	GTGAGAACT	GTGATTAAGT	CGATTAATCT

10	20	30	40	50	60	70	80
VMAFL	PTILNQLFRV	LTRATOEEVA	VVRVVIHV	VACCHEGLE	SHLSYVKA	YKAEPTVASE	YKIVHEELTK
ILKPSA	DFLTNSKLLR	YSWFFFDVLI	KSMAGHLIEN	SVKLLKQOR	FPASYHAAE	TVVNLMPHI	TQKQGNPEA
NMSLAV	FIKRCCTFMD	RGVFFQIDN	YISCFACQDF	KLIFYEYEF	LRVVOHREY	IPILKMPHFG	KGRIGRYQOL
SLTDEF	CRNHFLVGLL	LREVTALGE	FREVKLIAIS	VLOLLIKHS	FDERYASRSH	QARIATLYLP	LPGLLIENVQ
RDVSPF	PVNAGNTVGL	ESLALPAVNF	LVTPOKSTL	INSLKLDLIG	AISGLASPTT	TSTPNINSVR	KADSRGSLIS
INSLPER	NSEKNSLSDK	HOOSSTLGRS	VVRCDKLDQS	EIKSLIMCFL	YILKMSDDA	LFTYHMKAST	SELMOPFTIS
LHOFOYM	GKRTIARNGE	GLQPTVHGRK	SOTLPVSRFR	TOMGHARLQ	LGSLDNLSTF	NHSTYHSDAD	VLRHSLLEAM
EVCLTAL	DTLSLTLAF	KNQLLADHGH	NPLMKVFDV	YLCFLQKHQS	ETALQOVFTA	LRSLYKFFPS	ITFSGRADMC
CYEILAC	CNSKLSIRT	EASQLLYFLM	RNNFDYTGK	GFVRTHLQVI	ISVSQLLADV	VGIGETRFQ	SLSTHRCAN
LIKHTSF	SEDVKDLTKR	IRTVLMATQ	MKEHNDPEM	LVDLQYSLAX	SYASTPELRK	TWLDSHARLH	VKRGDLSEAA
VHVTALV	AEYLTKRGVF	ROGCTAFRVI	TPHLEDEAM	MEDVGNQVH	FNEDVIMELL	EQCAKELMKA	ERYELIADY
IPYTKR	RDFEDEDGK	EYIYKEPFLT	PLSEIQRLL	KLYSDKFGSE	NVMKIDSGK	VHPKDLDSKY	ANYQVTHVIP
JEKLOER	KTEFFERSHNI	RUPMFEMPT	QTGKQGGVE	EQCKRKILT	ALHCFPTVK	KIPVHYQHBT	DLRPLEVAID
KIVADLR	QLCSSAEVDN	IKLQKLGQS	VSVVWAGPL	ATARAFLDIT	NIRKYPDNV	ILLKEVTRFP	VEACQALAV
HLIKEDOL	EYQEDMKANY	REHAKELSEI	MHEQICPLEE	KISVLPWELH	IFKALSGTPT	STHWGHTSS	SSVV
10	20	30	40	50	60	70	80

FIG. 10E (cont.)

10	20	30	40	50	60	70	80
JATTGTAAATA	CGAGTCACTA	TAGGCGCAAT	TGGGTACCGG	GAGGTGAGCG	GTATCGATAA	GCTTGTATTC	80
JAATTTCGGCA	CGAGTTTTCAC	ACCATCAACA	AAACCCAGAA	TTTTATGATG	AGATTAAJAT	ACTCAGCTGC	160
GTGAJAAAGCA	CCACCTGTGTG	CTCACATCTC	TCAATGTGCA	CTGTGACACAC	TCAGGTAAJAG	GAAGCAGGAA	240
JTCGTTGAA	CCCAAGTTTGG	CTACTCTCTG	CTTCCCTCTG	TGAAGACGCG	AGAGGTTGTTG	ACAGAGGAGC	320
GGTCTTGGG	AACTCTTCTT	CGGCTATCTT	TGGCTACCCA	GAGTCTGGGA	TGGGCAGGCA	TATATGTCCT	400
GGGTAGATGG	AGGCAAGGCCA	CTGCTGAA	CTTCCACTCA	TCTGTCTTCT	ACAGAGATAC	TACAGTATCT	480
ATTTTITTTCA	GTACTGTGTG	AAACCCGAAT	GTGAGGCCA	AGCCTTAGGA	CCAGCTCTTC	CGATCTCTCA	560
CACTGGATATG	AGGACACAGT	GATGATTCCT	TTCTTGCCCA	CTATCTTAA	CCATGTGTTG	CCAGAGCCAC	640
ACAGGAAGAA	GTGCGGTTTA	AGCTGACTGT	GGTCAATTAT	CAATGTGTTG	CCAGTGGCCA	TGAGGAAGGA	720
ACTTGAAGCT	ATATGTTTAA	TACCGGTATA	AGGCTGAGCC	ATATGTTGCT	TCTGAATACA	AGACAGTGCA	800
ACCAATATCA	TGACACAGAT	TTCTCAAGCT	TGTCGGGATT	TCTCTACCGC	CACAAACTTA	CTGAGTGTCT	880
CTTTGATGTA	CTGATCAAA	CGGCTATCTT	GCATTGATA	GAGACATCCA	AAATTAAGTT	CTGCGGAAC	960
CTGCTACTCTA	TGATATGCA	TGACAGCTCT	TGTTAAATAT	GTGATGATGCA	CACATCACTC	AGAAATTTGG	1040
GAGGCACTTA	ACAAACGGGA	TGCTGATCTA	CTGCTCTCCA	TGAGAGGATG	TTTCACTCTC	ATGACAGGTT	1120
CAAGCGATTC	CAACCATGAA	CATTGTATTT	TGCTCTTGGA	CACCCCAAGA	CGCTTCTTGA	ATACAGATTT	1200
TGTTATGTTG	TTGACTACTC	ATTAACAGAT	GAATGTGCA	ACCAATGCCA	TTTGGAAAGC	CGAGGATTTA	1280
GACCTCCGAG	CAGGAGTTCC	GGGAGGTCG	TCTGATCGCC	GAACCTGCT	CTTGTGAGGA	CTTACTGATCA	1360
GACGCGCTTC	TGCTTCAAGG	AGGCACTCAG	CAGGATGAGC	CACCCCTCAC	CTGTGCTTCT	GTGATTAAGG	1440
ATGCAGGATA	TGATGTTGAG	GGAATGTGTA	CCCTTCTCTG	TGAAACCGGG	CATGACCTCT	AGAGTGTAAJ	1520
CTCCAGCTGTG	CCCTGCTCTG	TATGAGCTCT	GAGGCGAAGC	ACCCCTGACA	ACAGCTGTCA	CAGGAGCTCT	1600
TTCTCGGCACT	TGCTTCTCCA	CACATCTCAA	GAAGATGATA	CATCAACAGT	GTGAGAAATG	CTGATCTCAG	1680
ATCAGACAG	ATTTGCGTGG	TGCTGCTGTA	TAACTTGAC	GTGAGAGAG	CAATTCCTCT	GATGATGAGT	1760
CACATTTGGA	CATGCTGAT	GATGCTTTGT	TATCATATGT	GTGATGATG	TAAAGAGCTT	ACTGATGTCT	1840
ATATCTGAG	TGCTGCTCCA	CCAGTTTCAG	TACATGGGA	GATGATGATG	TACAGATCTC	AACTTATGGA	1920
AGTCACTGAT	CGAAGTCTCA	AGCATTTGCC	TGTTTCCGCT	GATGATGATG	CAAGGAGGCT	TGGAGCCCAT	2000
GGAGCTTGA	TAACTCTCTG	CTTTTAAAG	ACAGCTATGG	GATGATGATG	CAAGGAGGCT	TGGAGCCCAT	2080
GGCAACATTT	CTACTGAGCT	TGCTGTGCA	CTCTTGAGCA	CCACTGGGAC	GGAGATGTGT	TGCCACCATG	2160
GGCGACACT	GATCATTAAT	CTCTCAATGA	AAATGTTT	GGCTTCTCTT	ATTTACATGT	CTCTTTAAGA	2240
GGGCTTTAA	AAATGTTTCA	ACTGCTTTAA	GGTCTTTTAT	GAATGTCTAC	TGTTTCTTCT	TCAAJAAACT	2320
ATGTTGTGG	CTGTGTTCTA	CGAGATCTCT	AGTGTGCTA	TTATTAAGTTT	CCCTTAAACT	TCTATGTAAG	2400
CTGCTACTTC	CTGATGAGGA	ACAACTTTGA	TACATCTGGA	AGAAAGTCTT	GAGCTCTCAT	AGGCGGGAGG	2480
CTGTGAGCCA	CGTATGAGCA	CGATTTGTTG	CGATTGGGA	AACCAAGATT	CTGTGCTGAG	TGCTTCATAT	2560
GGCAACAGT	ACCGCTCTG	AGGCTTCTCT	GTGATGATG	CTGATGTGAA	GGACTTAACT	AAAGAGGATG	2640
AAATGCCAC	GGCCAGCTCT	AGGAGAGCTT	GGCTGAGCA	GAGATGCTGG	TGAGCTTACC	ATAAGGATCT	2720
CAAGCGATTT	GCTATGTTCA	GGTAAACAGG	CTAGTGGGAG	ATGCGGACAG	ATCCATGTCA	AAATATGGGA	2800
GGCCTTCAG	GTCAITTACC	CMAATCTGCA	CGAGGAGGCC	TCCATGTATG	ATGATGATG	GGAAAGGAGT	2880
ACGAGAGTT	GTGATGAGG	CTCCTTGAGC	AGTGCGGAGA	TGAGCTCTGG	AAAGCTGAGT	GTGATGATG	2960
GTATACAAAC	CTTATATCCC	CATTATATG	AGGCGGAGGG	ATTTCTTTTGA	AGATTAAGAT	GGAAAGGAGT	3040
GGACCGAA	CTACACGCT	TGCTGAGGA	ACCTTAAAG	CTCCTTAAAC	TGATCTCGGA	TAAATTTTGT	3120
TTAAANTGAT	ACAGATGTTA	GGCAAGTCTA	GAJAAAGGGA	TCTGGAATCT	AGATTAAGAT	ACATCTAGCT	3200
ATCCCTCTCA	TTAGGAAJAA	AGATTTGCA	CGAGGAGGGA	GGATTTTGA	GAGATTCACC	ACATCTAGCT	3280
CTTCCGATG	CCCTTATGTT	AGAAAGGCA	TCCCTGTCTAT	GTGAGGAGG	CGATCAACCT	TGAAACCCAT	3360
ATTGACGAGA	TGATTAAGAA	GGTGGCGAG	CTCCGCGAGC	TGTGCTCTCT	CCACTAGCAT	ATGCGGAGC	3440
CAATCTCAG	GTGATGAGG	GTGTTTCAAT	CAATCTCTGG	CACTAGCAT	AGTCTTCTAG	TTTCTTAGAT	3520
CAAGGCTCA	CTGATCAAT	AAAGTAAAG	CAGCTCTGAT	AGTCTTCTAG	CAATTTGAGG	AGCTTCTGCG	3600
GGGTAAAGC	AACTGTGAT	TAAAGAGAC	CTGCTCTCTG	ATCAGGAAGA	CAATTTGAGG	AACTCAAGGG	3680
GGAGCTTTCT	GAATCTATC	ATAGCAGAT	CTGCTCTCTG	GAGGAGGA	CGAGCTCTCT	ACCAATTTCT	3760
CTACGACCAT	CAGTGAGAT	CCACAGCA	CAATGTCTCT	CGAGTGAAC	AGCTCTCTCT	CGGTCTGTTG	3840
ATGCGCGGT	TGTTGGAGAT	TGCTTGTTCA	TTTGCJAACT	ACACAGCTCT	TCCGAAGCCA	ACTCTTCTAT	3920
CGAGGAGGAC	CAGGAGGAGG	GGGAGGGA	GGAAATTAAG	CAAGTCTTCT	ATGATGATG	CACTTCTATC	4000
AGAGAGTGA	CATATTTT	TAAATCTGAC	TGCTCAATAT	GTGTTAGATAT	AGATGGCTTA	CAGJAAJAA	4080
TCITGAGCTG	GACTTAGAT	TATTTCTCTC	TGTCAGATGA	GGGAGACTTT	TGCTCTGATC	CTGTCGGGAA	4160
ATATGATGTT	GGAGAGGCG	TGAGTTTCTC	TAGAGATATG	TTGATGATCT	AGGATTTTGT	CTATTTATCT	4240
ATACAGGTT	CAAGATCTAC	TACATGACT	TACATGACT	TJAATCCGCT	ACTGCTGCTA	AGTCAAGAT	4320
ATAGAGCAG	AAAGAGGCT	ATATGATAT	TACATGACT	CACTTTTAA	ACTCAACATG	GCTTATGAT	4400
TCATGCACT	CGAGCGGCT	CCAGTATATG	CAATACAT	TAAATGGTTA	TCTTGTGAT	AAAATGAGG	4480
TGTTGATAAT	TGTTACTG						4560
10	20	30	40	50	60	70	80
4598							



10	20	30	40	50	60	70	80
MLAFL	FTILNOLFRV	LTRATQEEVA	VNVTRVIRV	VACCHKGL	SHLSYVKA	YKAEPTVASE	YKTVHEELTK
10	20	30	40	50	60	70	80
MLPRA	DFLTSMKLLR	YSMFTFDVLI	ASNAQELIEN	SVVLLKWR	FPASYBUAAE	TVVWGLMPRI	TOKPGDNPFA
MSLAV	FIKRCFTFMD	RGFVFFQIRM	YISCFAPKDF	KILFEYKFEF	LRVVOBHEHY	IDLKLPMPFG	KGRICRYQDL
SLDEF	CRNHFLVGLL	LAUEVGTALGE	FREVRLLAIS	VLOELLKHS	FDERYASRSH	QARIATLYLP	LPGLLIENVQ
ADVSPF	PVNAGMTVKD	ESIALPAVNP	LVTPOKSTL	ENSLKIDLLG	AISGLASPTT	TSTPTNINSVR	NADSRGLIS
NSLPER	NSEKSNSLDK	HQOSSTLGRS	VVRCDKLDQS	EIKSLIMCFL	YILKMSDDA	LFTYMKAST	SLKMPFTIS
HQFOYM	GKRYIARNOE	GLSPYVHGRK	SOTLPSVRRR	TOMGUALQO	LGSLINSITP	RHSYGHSDAD	VLRGLILEAN
VCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKAFTIV	YLCFLQKHQS	ETALKNVFTA	LRSLITYKFFS	TFYGRADMC
YEILKC	CNSKLSSEKT	EASQLLYTLM	RNNFYTGKK	SPVRLQLQVI	ISVSQLIADV	VGIGETRFQO	SLSTIRNCAN
IKHTSF	SSVVELITKR	IRTVLMTATM	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	EQCADGLAKH	VKXGLLESA
QVITALV	AEYLTRUGVF	ROGCTAPFVI	TPHIDEASM	MEDVGRQDVH	FREDVIMELL	VHPKIDLSKY	AYIQVTHVIP
PIYKKA	KDFTEDDGK	EYTYKEPKLT	PLSEISORLL	KLYSDKFGSE	NVXMIQDSCK	RIFPMVQHHT	DLAPIEVAID
HELGER	KTEFERSHRI	RUFHFEPPT	QTGKRGQGV	EOCHRTILT	ALNCHFTYVK	KLKKEVFRFP	VEACQCALAV
KVAKEL	QLCSSAEVDM	IKLQJLQOQS	VSVOVNAGFL	AYARAFLOUT	NTRYPERHKV	SSVV	1194
LKEDOL	EYQEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNLSH	IFHLSGTPT	STMVHGHTSS	SSVV
10	20	30	40	50	60	70	80

FIG. 10F (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAAAT	CGACTCACTA	TAGGCGAAT	TGGGTACGG	GGCCCCCCTC	GAGGTGCGAG	GTATGATGAC	GCTTGATATC
81	GAATTGGCGA	CGAGTTTATC	ACCATCACA	AAACCCGAGA	TTTTTATGAT	AGATTAAAT	AGAGTTGACC	ACTCAGCTGC
161	ATGMAAAGCA	CCACCTGTGT	CTCACTATCT	TCCATGTCAG	CTGTGACAC	TCAATGATG	GAGACAGCAA	GAAGAGGGAT
241	GTGCTTGAAA	CCCAAGTTGG	CTACTCTCTG	CTTCCCCCTC	TGAAGAGGAG	AGAGGTGTGT	ACAGCGGAGC	GAATTAATAT
321	GGTCTGGCGG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGCGAGCGA	TTATGTTCCG	GAATTAATAT
401	GGGTAGATGT	AGGCAAGCGA	CTGTGTAARA	TTTCACTCA	TCGTGTTTCT	ACAGGGATCT	TCAGATGATC	CATTTCATCA
481	ATTTTITTCGA	GTACTGTGAT	GAATGTGGC	GGTCAATATT	AGCCTTAGGA	AACGAATCTT	TAAATGACTT	TAAGAGTCTG
561	CATGGCGATG	AGGCCACAGT	GTATGTGGC	TTCTTGUCCA	CTATCTTAAA	CCAGCTGTTC	CGAGTCTCCA	CCAGAGGCCA
641	ACAGGAAGAG	GTGCGCGTTA	ACGTGATCA	AGGCTAGGCC	ATATGTTGCC	TTCTGATGCA	AGACAGTGTG	TGAGAGAGCT
721	ACTTGGAGGT	ATATGTTTAA	CTGCTATATT	GGTCAATATT	TCCTTCAACGA	CTAAGCACTA	CTGAGGATCT	CATTGGTTTCT
801	ACCAATATGA	TGACCACTGA	TTCTCAAGCTT	TCGTGCGGAT	TCCTTCAACGA	CTAAGCACTA	CTGAGGATCT	CATTGGTTTCT
881	CTGATTTGTA	CTGATCAAA	CTATGTCCT	GCATTTGATA	GAGAATCTCA	AGTTTAAAT	GCTGTGAAAT	AGAGGATTTCT
961	CTGATCTCTA	TCATCATGCA	GGGGAAAGCC	TTGTAAATAT	GCTGTATGCC	CACATCACTC	AGAGTGTTCG	AGATTTATCT
1041	GAGGCACTGA	AGAACGCGAA	TATAGTACCT	GCTGCTCTCA	TCAGAGGATG	TTTCACTCTT	ATGACAGGAG	GCTTTTGTCT
1121	CAGACAGCTC	ATCACTACTA	TTACTGTGTT	TGCTCTCTGA	GACCCAAAGA	CCCTCTTTGA	ATACAGATTT	GAATTTCTCT
1201	GTGTAGTGTG	CAACCATGAA	CATTATATC	CTCAAGACTT	ACCAATGCCA	TTTGGAAAA	CGAGGATTTA	AAGATACCAA
1281	GACCTCCAGC	TTGACTACTC	ATTAACCTCG	GAGTGTGCGA	GACAAACACT	CTTGTGAGGA	CTTGTACTGA	GGGAGGTGGG
1361	GACAGCCCTC	CAGGAGTCTC	GGGAGGTGGG	CTGTATGCGC	ATCATGTGTC	CTGCTCTGCT	CTGTATTAAG	CCCTGCTCTC
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTTAC	CTGCTCTGCT	CATTCTTTTG	CCCTGCTCTC
1521	GTTCAGCGGA	TCATATGTAG	GGATGTGTCA	CCCTTCCCTG	TGAACCGCGG	CATGCTGCTG	AAGGATGAAT	CTTGTAAAGT
1601	ACACGCTGTG	ATATCCGCTG	TGAGCGGTGA	GAAGGGAAAG	ACCTGTGACA	CACAGCTGCA	CAAGGAGCTG	CTGGCGGTCT
1681	CTTCCGCGAT	TCCTTTTCCA	TATCAACCT	CAACTTCCAA	CATCAACAGT	GTGAGAAATG	CTGATGTAGG	AGGATCTCTC
1761	ATACATCTGA	ATTTCGGTTA	CAGCCTTCCA	GAATTAATAT	GTGAGAGAGG	CAATTCCCTG	GATTAAGCAG	CAAAAGATGT
1841	CAGCTTGGGA	AATTCCTGTT	TGCTGCTTGA	TAAACTTGG	GTGAGAGAGG	CAATTCCCTG	ACTGATGTGT	TTTCTCTACA
1921	TTCTTAAAGG	CATGTCTGAT	GATGCTTTGT	TTACATATTG	GAACAGAGGT	TCACATCTCT	ACATTTGAGA	AGAGCCCATC
2001	ATATCTGATG	TCGTGCTGCT	CAATTTCCAG	TACATGCGGA	AGCAGATACAT	AGCCAGAGAC	CAGGAGGAGT	CAGGAGGAGT
2081	AGTTTCTGAT	CGAAGATCTC	AGACATTTGCC	TTTTTCCGCT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGGAGGAGT
2161	GGGCGCTTGA	TTACTCTCTC	ACTTTTAACT	GCTCTGAGCA	CCACTGGGAC	GAATGATGTC	CGCTCAAGTC	ATTACTTGA
2241	GGCCACATGT	CTACTGAGGT	TTGCTGCTGC	CTCTCATGAA	GAAGATTTCT	ATTTACATTG	GGTTTAAAGA	ACCACTGCTT
2321	GGGCGGACAT	GGACATATCT	CTCTGCTTAA	GGTCTTAAAT	GATGCTTACC	TCGTTTAACT	TTCTTAAAGT	TCGTTTAAAGT
2401	GGCTTTTAAA	AAATGTGCTT	GGTCTTAAAT	GGTCTTAAAT	TTTAAAGTTT	CTGTTTAACT	TCGTTTAAAGT	TCGTTTAAAGT
2481	ATGTTGCGGG	CTCTGTTGTA	CGAGATTCTC	AAATGTGCTT	ACTTCCAGCT	GAGCTCCACT	AGAGCGGAGG	CTCTCCAGCT
2561	GCTCTACTCT	GCTGTATGGA	GAGTTTGTG	TTACACTTGA	GAAGAGTCTG	TTTGTCCGCT	ACATTTGAGA	GTCTACTATA
2641	CTGTACAGCA	CTGTATGAGA	GAGTTTGTG	TTACACTTGA	AACCCAGTCT	CAGCTCCACT	AGAGCGGAGG	GTCTACTATA
2721	GGCCACAGCT	ACCGGCTTAT	TAGCACACCT	GAAGAGTCTG	GAAGAGTCTG	CAGCTCCACT	AGAGCGGAGG	GTCTACTATA
2801	AATGGCCACC	GGGCGGATCT	AGGAGAGCTG	GGCTGACAGC	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
2881	ATGCGACAGC	GGGCGGATCT	AGGAGAGCTG	GGCTGACAGC	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
2961	GGGCAATGAT	GCTATGTGCA	CGTAAACAGT	CTAGTGGGAG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3041	GGGCAATGAT	GCTATGTGCA	CGTAAACAGT	CTAGTGGGAG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3121	ACGAGGATGT	GCTATGTGCA	CGTAAACAGT	CTAGTGGGAG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3201	ATCTACACAT	TTTACTATCC	CATTATTGAG	TTCTTCAAGG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3281	GGAAACCAAA	CTCACACGCT	TTCTTCAAGG	TTCTTCAAGG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3361	TCAAAATGAT	ACAGAGTTCT	GGCAAGTCTA	ACCTTAAAGA	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3441	ATCCCTCTCT	TTTACAGAAA	AGAGTTTCCA	GAAGAGTCTA	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3521	TGAGATGACA	CTGCTGAGCA	CGGAGGAGCT	GGAGGAGGAG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3601	CTGCTGAGCA	CTGCTGAGCA	CGGAGGAGCT	GGAGGAGGAG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3681	ATTGACGAGA	TGAGTAAAGA	GGTGGCGAG	TTCTTCAAGG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3761	CAAACTGAGT	GGGCGGATGA	GGTTCAGGCT	CAATCTGAGC	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3841	CAAACTGAGT	TCCTGACAT	AAAGTGAGG	TGCTTAAAGA	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
3921	GGGTTAAAGG	CACTGCTGAT	TAAAGAGAGC	TACGCTGAGT	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4001	GGGTTAAAGG	CACTGCTGAT	TAAAGAGAGC	TACGCTGAGT	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4081	TGAGGAGCAT	TTGCTGCTG	TGCTTGTGTA	TTGCTGCTG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4161	ATGCGCGCTG	TTTGGGAGCT	TTGCTGCTG	TTGCTGCTG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4241	CAGGAGGAGC	CAGGAGGAGC	GGGAGGAGC	GGGAGGAGC	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4321	AGAAAGTCTA	CATATTTTCT	TAAATCTGAC	TGCAATATAT	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4401	TTCTGAGCTG	GACTTATGAT	TTACTTCTCC	TTGCAAGATG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4481	ATCTACATGT	CAGGAGGAGC	TGACTCATGA	TTGATGCTGT	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4561	AATTCGAGCT	CAGAGCTTAC	TACTAGGACT	TACTAGGACT	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4641	ATGAGGAGCT	CGGAGGAGCT	CGGAGGAGCT	CGGAGGAGCT	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4721	TGCTAGCTCT	CGGAGGAGCT	CGGAGGAGCT	CGGAGGAGCT	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4801	TGTTGATAAT	TTTGTGCTGT	CGAGTATATG	CGAGTATATG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
4881	TGTTGATAAT	TTTGTGCTGT	CGAGTATATG	CGAGTATATG	GAATTTGAGA	GGACTTAACT	AAAGAGTCTG	GAAGAGTCTG
	10	20	30	40	50	60	70	80

	10	20	30	40	50	60	70	80
1	MEGHVMAI	PTILNQLFRV	LTRATQEEVA	VWVTRVVIHV	VAQCHIEDGLE	SHLSRYVYKA	YKAEPPYVASE	YKTVHEELTK 80
81	SMITILKPSA	DFILTSNKLK	YSNFFFDVLI	KSMQOHLIEN	SKVILLRNOR	FPASYNBAAE	TVVNMIMPHI	TOKPGUNPEA 160
161	SKNANHSLAV	FIKCFYFMD	RGFVFKQINN	YISCFAPGDP	KTILFEYKFEF	LRVVCNHEHY	IPLNLMPPFG	KGRICRYQDL 240
241	OLDYSLTDEF	CRNHFVLVGL	LRVFTALQE	FREVLLIAIS	VLNKLLIKHS	FDDRYSRSH	QARIATLYLP	LPGLLIENVQ 320
321	RINVRVPSPE	PVNAGNTVKD	ESLALPVPNP	LVTPOKGSTL	DNSLHKDLG	AISGLASPTT	TSTPHINSVR	NADSRGSLIS 400
401	TDGNSLPER	NSEKSNSLDK	HQOSSTLGNS	VVRCDKLDOS	EIKSLIMCFL	YILKMSDDA	LEFTWNAKST	SELMDFFTIS 480
481	EVLCHOPQVM	GKRYIARNOE	GLGPIVHDRK	SQTLPSVRNR	TGMMHARLOQ	LGSLDNSLTF	NHSTGHSDAD	VLHQSLLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFIV	YLCFLQKHQS	ETALKNVFIA	LASLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSLIRT	EASQLLYPLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRPQO	SLSIINNCAN 720
721	SDRLIGHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LYDLQYSLAK	SYASTPELRK	TWLDSEMARH	VKNGLDSEAA 800
801	MCVVHVTALV	AEYLTRKGVF	ROGCTAFKVI	TPKIDDEASH	MEVGMQOVH	FREDVLMELL	EQCADGLWKA	ERYELIADTY 880
881	KLIIPYIEKR	RDFFEDEDGK	EYTYKEPKLT	PLSEISQRL	KLYSDKFGSE	NVIMQDSGK	VNPKDLSKY	AYIQVTHVIP 960
961	FFDEKELQER	KTFERSHNI	KRFMFEMPTT	OTGKROGQVE	EOCKRRITLT	AHICFPYVKK	RIPVMYOHMT	DLNPTEVAID 1040
1041	ENSKVVAELR	QLCQSSAEVDM	IKLQLEQGS	YSQVQVAGPL	AYARAFLEDT	NTKRYPDNKK	KILKEVPROF	VERACQALAV 1120
1121	NERLIKEDQL	EYQEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPP	STMVHGNTSS	SSVV 1194
	10	20	30	40	50	60	70	80

Flt. 106 (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAAATA	CGACTCACTA	TAGGCGGAAT	TGGGTACGGG	GGCCGCCCCC	GAGGTGAGAG	GTATGTGATGA	GCTTGTATATC
81	GAATTGGCGCA	CGAGTTTTCAC	ACCATCACCA	AAACCAGGAA	TTTTTATGAT	AGAGTTGATCC	ACTCAGGTGTC	1860
161	ATGAAAGAGCA	CCACCTGTTTG	CCATCATTTCT	TCCATGTTCAG	CTGTGACAACT	TCAAGTAAAG	AGAGTACGAA	GAAGAGGGATG
241	GTCTGTGAA	CCCAAGTTGTC	CTGACTCTGG	CTTCCCTCTC	TGAAGAAGACG	AAAGGTTGTTG	ACAGCGAGAG	2420
321	GGTCTGGGG	ACACTTTCTCT	CGGGCTATCT	CGGCTATCTC	TGGCTACCAA	TGGCTACCAA	TATATGTTCCG	3230
401	GGGTGATGG	AGGCAAGGCA	GTGCTGAA	TTTCCCACTCA	TCGTGTTTCT	ACAGGGATAC	TCAAGTATCAG	CATTACTACTC
481	ATTITTTTCCA	GTACTGTTCAG	GAGTGTGCG	TCCTGAGTCA	AGCCTTAGGA	AAAGAACTCT	TAAATTAACCT	TAAGAGTCTTG
561	CATGTGGATCG	AGGCCACAGT	GATGATCTCC	TCCTGAGTCA	CGAGGATAC	CGAGGATAC	CGAGGATAC	5620
641	ACAGGAAGAA	GTGCGGGTGA	AGGTGATCTC	TCCTGAGTCA	CGAGGATAC	CGAGGATAC	CGAGGATAC	6420
721	ATCTGAGGTC	ATATGTTTAA	TACGCTGATA	AGGCTGAGCC	CGAGGATAC	CGAGGATAC	CGAGGATAC	7230
801	ACCAATTCCTA	TGACCAAGAT	TCCTGAGGCT	TCCTGAGGCT	TCCTGAGGCT	TCCTGAGGCT	TCCTGAGGCT	8040
881	CTTGTGATGA	CTGATCAATTA	CTATGGCTGA	GCATTTGATA	GAGAACTCCA	GCATTTGATA	GCATTTGATA	8850
961	CTGCATCTTA	TCATCATGCA	GGGGAAGACG	TGTTAAATAT	GCTGATGCCA	CACATCACTC	AGAGTTTGGG	9660
1042	GAGGCACTTA	AGAACCTGAA	TGATGAGGCT	CGTCTCTTCA	TCAAGAGATG	TTTCACTTCT	ATGAGACAGG	10470
1121	CAGGCAAGTC	AAACAATGAA	CTGATGCTTT	TGCTCTCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAGATTT	11280
1201	GTGTAGTTGTG	CAACCATCTAC	CATTATATTC	TGCTCTCTGGA	ACCAATGCTCA	TTTGTGAAAG	CAGAGGATGA	12090
1281	GACCTCCAGC	TGACTACTTC	ATTACAGAT	GAGTTTGCA	GAAGAACTCT	CTTGTGGGGA	CTTTTATCTA	12800
1361	GACAGCCCTC	CAGAGGATCC	GGGAGTCCG	TCGTGATGCC	CACTCTCTAC	CTTGTGGGGA	CTTTTATCTA	13610
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACTCTCTAC	CTTGTGGGGA	CTTTTATCTA	14420
1521	GTCCAGCGGA	TCATGTGTAG	GAGTGTGTTA	CCCTTCCCTG	TGAGCGGGGG	CATGACCTCG	CAAGGATAGC	15230
1601	ACGAGCTGTG	AATCCGCTGG	TGAGTGTGTT	CCCTTCCCTG	ACCTGCTGAG	CACAGCTCTG	CAGGAGCTGT	16040
1681	TCCTCGCATC	TGCTTCTGCA	GAATTAAGCT	CAACTCTCAA	CATCAACAGT	GTGAGAGAGG	GTGAGAGAGG	16850
1761	ATAAGCAAGC	ATTGCGGTAA	CAGCTCTTCA	GAAGAGATA	GTGAGAGAGG	GTGAGAGAGG	GTGAGAGAGG	17660
1841	CACATTTGGA	AATTCCTGTT	TGCTGTGTTA	TAACTTTGAG	GTGAGAGAGG	GTGAGAGAGG	GTGAGAGAGG	18470
1921	TCCTTAAAGAG	CATGTCTGAT	GAGCTTTTGT	TTATCATATT	GTGAGAGAGG	GTGAGAGAGG	GTGAGAGAGG	19280
2001	ATTATCTGA	TCGTCTGCTG	CAATGCTTCA	TACATGATTT	GTGAGAGAGG	GTGAGAGAGG	GTGAGAGAGG	20090
2081	AGTTCATGAT	CGAAGGTCTC	AGACTTATGC	TGTTTCCGCT	GTGAGAGAGG	GTGAGAGAGG	GTGAGAGAGG	20800
2161	GAGGCTGTGA	TAAGCTTCTC	ACTTTTAACT	CAAGCTATGG	GTGAGAGAGG	GTGAGAGAGG	GTGAGAGAGG	21610
2241	GCCACATATT	CTACTGAGGT	TGCTGTGATA	GCTCTGAGCA	CAAGCTATGG	CAAGCTATGG	CAAGCTATGG	22420
2321	GCGCGACCAT	GGACATATTC	CTCTCATATG	AAAGTATTTT	CGCTTCTCTT	ATTATCATAT	GGTTTTAAAG	23230
2401	CGGCTTTAAA	AGATCTAATC	ACTGCGTTAA	GGTCTTTAAT	GTGATCTTAC	TGTTTCTTCT	TCAAAAACCT	24040
2481	ATGTGTGGGG	CTCTGTGTTA	CGAGATTTCT	AGTGTCTGTA	TTATAGATTT	CCCTCAAGAT	TCTATGAAGG	24850
2561	GCTCTACTCT	TGATGTAGGA	CAACTTTTGT	GCATTGCGGA	ACTCCAGACT	GAGTCCCAT	AGGACCGAGG	25660
2641	CTGTGACCA	GCTGTAGGCA	AGATTTTGTG	TTACACTGGA	AGAAAGTCTT	TTGTGCTGAC	ACATTCCGAC	26470
2721	GCCACAGATG	ACCGGCTTAT	TAAGCAACAT	AGCTTCTCTT	AACCAAGATTC	CAGCAGTCCC	TGTCATCATC	27280
2801	AATGGCCACC	GCCACAGATG	AGGACATGTA	GAAGCACCA	CTGATGTGAA	GAGCTTAAAC	AAAGAGATAC	28090
2881	ATGCCAGCAG	GCCGAGGCTC	AGGAGAGCTG	GGCTGACAG	GAGATGCTGG	TGACACTCCA	GTACAGCTGC	28800
2961	GGAGCAATGC	GCTATGTGCA	GTTAACAGCT	CTAGTGGCAG	CATGCGCCAG	ATGACCTATCA	TTCTCTCAGG	29610
3041	CGCTTCTCAG	GTGATTAAGC	CAAACTATGA	CGAGGAGGCC	TCCATGATGG	AGAGCTGAGG	GATGCGAGCT	30420
3121	ACGAGGATGT	GCTGATGAGG	CTCTTTGAGG	AGCGGCGGAG	TGGACTCTGG	AGAGCGCGAG	GTGAGAGAGG	31230
3201	ATTCTCAAAC	TATCATCTCC	CATTATGAG	AGCGGAGGCC	ATTCTTTTGA	AGATGAGAGT	GGAAAGAGCT	32040
3281	GGAAACCAAA	CTCACACCTG	TGTCGGAAGT	TTCTGAGGTA	TCCTTTAAAC	TGTACTGAGA	TAAATTTGGT	32850
3361	TCAAAATGAT	ACAGAGTTCT	GGCAGGTGTA	ACCTTAAGTA	TCTGTTAAAC	AGATTAAGAT	ACATTCAGAT	33660
3441	ATCCCTTTCT	TTGACGAAAA	AGAGTTGCAA	GAAGGAGAAA	TCTGTTAAAC	AGATTAAGAT	ACATTCAGAT	34470
3521	TGAGTGCCCA	TTTACGAGCA	CGAGGAGGCC	GCAGGCGGGG	CGAGTTTGA	AGCTTATGAG	AGCTTATGAG	35280
3601	TACACTTTCT	CCCTTATGTT	AGAGAGGCCA	TCCCTGTGAT	GTGAGAGAGG	AGTCAAAAGC	AGTCAAAAGC	36090
3681	ATTGAGAGAG	TGAGTGAAGA	GGTGGCGAG	CTAGTGGGCT	GTACAGGAGC	CACACTGAGC	TGAACCCCTC	36800
3761	CAAACTCCAG	GCGAGCTGTA	GGCAGGTGTA	ACCTTAAGTA	TGTCCTCTCT	GGGCGAGGCT	GACATGATCA	37610
3841	CAAGGCGATA	TCTGACATAT	AAAGTGAAGC	CACTGCTGGC	CCACTAGCAT	ATGCGGAGGC	TTTCTTGAAG	38420
3921	GCGTTAAAGC	AACTGCTGAT	TAAAGAGAGC	CAGCTGCTGC	AGCTTTTGAAG	AGCTTTTGAAG	AGCTTTTGAAG	39230
4001	GGAGCTTTCT	GAATATGATC	ATGAGGAGAT	GTCGCCCTCT	AAAGTGAAGC	AAAGTGAAGC	AAAGTGAAGC	40040
4081	TCAGACCCAT	CAGTGGGAGC	CGAAGAGGAA	CAATGGTTCA	GAAGAGAGG	CGAGCTCTCT	CGGTGCTGTT	40850
4161	ATGGGCGGAG	CGAGGAGGAG	TGCTTTGTTA	TTTGCAAACT	CGGAGTGAAT	TCCAAAGGCA	ATACCTCTCT	41660
4241	AGAGGTTGCA	CATATTTTCT	TGAGGAGGAA	GGAAATTAAG	AACAACTGTT	TTCTTTTAAAC	GACTTTCTAT	42470
4321	CTTGTAGGTC	GACTTGAATT	TTATCTCTCT	TTCGAGATTA	CAAAAGTTTCT	ATGTGTTGTT	ACAAGAGGTT	43280
4401	ATCTCATAGT	CAGGAGGGGC	TGCTGAGTCA	TTGATGCGCT	GTGTTAGATT	AGTGGGCTTA	CAGAAAJJJA	44090
4481	AATCAGGTTA	CAGAACTTAC	TAGTTTTGTG	TAGAGGATAT	AGGAGGACTT	TGCTCTGAGT	CGTGGCGGAA	44800
4561	ATGAGCAGAG	AATAGTGAAC	TAGTGAAGCT	GACACTCAAA	TTTATGAGCT	CTATATCTCT	CTATATCTCT	45610
4641	TCATGAGCTT	CGGAGGCGCT	ATATATGAT	TACATTTCTA	CATTTTTAAAT	ACTCAGATGC	GCTTATGATG	46420
4721	TGTGATAAAT	TGCTGTCTGT	CCAGTATATG	CAATACACTT	TAAATGGTTA	TCTTCTGAT	AAATATGTGC	47230
4801	TGTATACATA	TCTTTACT						48040
4881								48890

FIG. 10H

	10	20	30	40	50	60	70	80
1	MEGHVNIATL	PTILNQLFRV	LTRATQEEVA	VWVTRVILHV	VAQCHEEGLE	SHLRSTYKVA	YKAEPTVASE	YKTVHEELTK 80
81	SMITILKPSA	DFILTSNKLIR	YSMFFFDVLI	KSMAGHLIEN	SKVKLLRNQR	FPASTYHAAE	TVVNLMPHPI	TQKPGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNREHY	IPLNLMPFG	KGRIQRYOBL 240
241	QLDYSLTDEF	CRNHFVLGLL	LREVGTAQCE	FREVRLIAIS	VLNLLIKHS	FDROYASRSH	QARIATLYLF	LPGLLIENVQ 320
321	RINVRDVSPP	PVNAGMTVKD	ESLALPAVNP	LVTPOKSTL	DNSLHKDLIG	AISGSIASPT	TSTPHINSVR	NADSRGSLIS 400
401	TDGNSLPER	NSEKSNLSDK	HQOSSTIGNS	VVRCDKLDQS	EIXSLIMCPL	YILKSMSEDA	LFTYMNKAST	SELMDFPTIS 480
481	EVCLHQFOYM	GKRYLARNOE	GLGPIVHDRK	SQTLFVSRNR	TGPHARLQQ	LGSLDLSLTP	MHSYGHSDAD	VLHQSLLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFV	YLCFLQKHQS	ETALKNVFITA	LRSLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSSIRF	EASQLLYFLM	RNFDTYIGKA	SPVKTHLQVI	ISVSQLIADV	VGIGETAPQQ	SLSLINRCAN 720
721	SDRLIGHTSF	SSDVKDLTKK	IRTVLMAIAQ	MKEHENDPEM	LVDLQTSIAK	SYASTPELRK	TWLDSPARKH	VKAKDISEAA 800
801	MCTVHTALV	ARYLTRGRVF	RQCGTAPRVI	TPNIDEEASM	MEVGMQDVH	FNEDVIMELL	EQCADGLWKA	KRYELIADIV 880
881	KLIPIIYEKR	RDFEDEDGK	EYIYKEPKLT	PLSEISORLL	KLYSDKFGSE	NVMIMQDSGK	VNPKDLDSKY	AYIQVTIVIP 960
961	FFDEKELEQR	KTEFERSHNI	RRPMFEMPTT	QTGKROGGVE	EQCKRFTILT	AIHCFPYVEK	RIPVMYQHYT	DLNPIEVAID 1040
1041	EMSKFVAELR	QLCSSAEVDM	IKLQKLGQS	VSVQVAGFL	AYARAFIDET	NTRYPDNFK	KLKKEVPROF	VEACGQALAV 1120
1121	NERLIKEDQL	EYQEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPSLSH	IFNAISGTPP	STMVHGMTSS	SSVV 1194
	10	20	30	40	50	60	70	80

Fig. 10H (cont.)

Exon 1A (-182 to -102)

GCAGGGGAAAAACCTGGCCCCATGATTCACCTTACTTCCCACCGGATCTCTCCCATGACACGTGAGGATTA  
TTACAATTTAA -102

Exon 1B (-219 to -102)

TTATCCCTTTACTACTTGCGAAGTGAGTTCGGTAGATGGGAGTGGAGAAGAGAACCTTAGAATCATTGTTTAGTCTTCAT  
CTTTCACAGCTCAGGCTGAAGGCCCTTCTCTGCTGAGA -102

Exon 1C (-143 to -102)

GCGGCAGAGCGTGTCTGAGGTGGTGC GCGGCTCCGTGCTCCT -102

Exon2 and the rest of human CLASP2 cDNA

-101 -79  
GGCAAAGCCAAAGCTAATTGAGC

-78 -1  
AAGCTAATTGAGCCACTCGACTATGAAAATGTCATCGTCCAGAAGAAGACTCAGATCTGAACGACTGTTTACGGGAG

1/1 31/11  
ATG CTG CTC TTC CCT TAC GAT GAC TTT CAG ACG GCC ATC CTG AGA CGA CAG GGT CGA TAC  
Met leu leu phe pro tyr asp asp phe gln thr ala ile leu arg arg gln gly arg tyr

61/21 91/31  
ATA TGC TCA ACA GTG CCT GCG AAG GCG GAA GAG GAA GCA CAG AGC TTG TTT GTT ACA GAG  
ile cys ser thr val pro ala lys ala glu glu glu ala gln ser leu phe val thr glu

121/41 151/51  
TGC ATC AAA ACC TAT AAC TCT GAC TGG CAT CTT GTG AAC TAT AAA TAT GAA GAT TAC TCA  
cys ile lys thr tyr asn ser asp trp his leu val asn tyr lys tyr glu asp tyr ser

181/61 211/71  
GGA GAG TTT CGA CAG CTT CCG AAC AAA GTG GTC AAG TTG GAT AAA CTT CCA GTT CAT GTC  
gly glu phe arg gln leu pro asn lys val val lys leu asp lys leu pro val his val

241/81 271/91  
TAT GAA GTT GAC GAG GAG GTC GAC AAA GAT GAG GAT GCT GCC TCC CTT GGT TCC CAG AAG  
tyr glu val asp glu glu val asp lys asp glu asp ala ala ser leu gly ser gln lys

301/101 331/111  
GGT GGG ATC ACC AAG CAT GGC TGG CTG TAC AAA GGC AAC ATG AAC AGT GCC ATC AGC GTG  
gly gly ile thr lys his gly trp leu tyr lys gly asn met asn ser ala ile ser val

361/121 391/131  
ACC ATG AGG TCA TTT AAG AGA CGA TTT TTC CAC CTG ATT CAA CTT GGC GAT GGA TCC TAT  
thr met arg ser phe lys arg arg phe phe his leu ile gln leu gly asp gly ser tyr

421/141 451/151  
AAT TTG AAT TTT TAT AAA GAT GAA AAG ATC TCC AAA GAA CCA AAA GGA TCA ATA TTT CTG  
asn leu asn phe tyr lys asp glu lys ile ser lys glu pro lys gly ser ile phe leu

481/161 511/171  
GAT TCC TGT ATG GGT GTC GTT CAG AAC AAC AAA GTC AGG CGT TTT GCT TTT GAG CTC AAG  
asp ser cys met gly val val gln asn asn lys val arg arg phe ala phe glu leu lys

541/181  
 ATG CAG GAC AAA AGT AGT TAT CTC TTG GCA GCA GAC AGT GAA GTG GAA ATG GAA GAA TGG  
 met gln asp lys ser ser tyr leu leu ala ala asp ser glu val glu met glu glu trp

601/201  
 ATC ACA ATT CTA AAT AAG ATC CTC CAG CTC AAC TTT GAA GCT GCA ATG CAA GAA AAG CGA  
 ile thr ile leu asn lys ile leu gln leu asn phe glu ala ala met gln glu lys arg

661/221  
 AAT GGC GAC TCT CAC GAA GAT GAT GAA CAA AGC AAA TTG GAA GGT TCT GGT TCC GGT TTA  
 asn gly asp ser his glu asp asp glu gln ser lys leu glu gly ser gly ser gly leu

721/241  
 GAT AGC TAC CTG CCG GAA CTT GCC AAG AGT GCA AGA GAA GCA GAA ATC AAA CTA AAA AGT  
 asp ser tyr leu pro glu leu ala lys ser ala arg glu ala glu ile lys leu lys ser

781/261  
 GAA AGC AGA GTC AAA CTT TTT TAT TTG GAC CCA GAT GCC CAG AAG CTT GAC TTC TCA TCA  
 glu ser arg val lys leu phe tyr leu asp pro asp ala gln lys leu asp phe ser ser

841/281  
 GCT GAG CCA GAA GTG AAG TCA TTT GAA GAG AAG TTT GGA AAA AGG ATC CTT GTC AAG TGC  
 ala glu pro glu val lys ser phe glu glu lys phe gly lys arg ile leu val lys cys

901/301  
 AAT GAT TTA TCT TTC AAT TTG CAA TGC TGT GTT GCC GAA AAT GAA GAA GGA CCC ACT ACA  
 asn asp leu ser phe asn leu gln cys cys val ala glu asn glu glu gly pro thr thr

961/321  
 AAT GTT GAA CCT TTC TTT GTT ACT CTA TCC CTG TTT GAC ATA AAA TAC AAC CGG AAG ATT  
 asn val glu pro phe phe val thr leu ser leu phe asp ile lys tyr asn arg lys ile

1021/341  
 TCT GCC GAT TTC CAC GTA GAC CTG AAC CAT TTC TCA GTG AGG CAA ATG CTC GCC ACC ACG  
 ser ala asp phe his val asp leu asn his phe ser val arg gln met leu ala thr thr

1081/361  
 TCC CCG GCG CTG ATG AAT GGC AGT GGG CAG AGC CCA TCT GTC CTC AAG GGC ATC CTT CAT  
 ser pro ala leu met asn gly ser gly gln ser pro ser val leu lys gly ile leu his

1141/381  
 GAA GCC GCC-ATG CAG TAT CCG AAG CAG GGA ATA TTT TCA GTC ACT TGT CCT CAT CCA GAT  
 glu ala ala met gln tyr pro lys gln gly ile phe ser val thr cys pro his pro asp

1201/401  
 ATA TTT CTT GTG GCC AGA ATT GAA AAA GTC CTT CAG GGG AGC ATC ACA CAT TGC GCT GAG  
 ile phe leu val ala arg ile glu lys val leu gln gly ser ile thr his cys ala glu

1261/421  
 CCA TAT ATG AAA AGT TCA GAC TCT TCT AAG GTG GCC CAG AAG GTG CTG AAG AAT GCC AAG  
 pro tyr met lys ser ser asp ser ser lys val ala gln lys val leu lys asn ala lys

1321/441  
 CAG GCA TGC CAA AGA CTA GGA CAG TAT AGA ATG CCA TTT GCT TGG GCA GCA AGG ACA TTG  
 gln ala cys gln arg leu gly gln tyr arg met pro phe ala trp ala ala arg thr leu

571/191  
 631/211  
 691/231  
 751/251  
 811/271  
 871/291  
 931/311  
 991/331  
 1051/351  
 1111/371  
 1171/391  
 1231/411  
 1291/431  
 1351/451

1381/461  
TTT AAG GAT GCA TCT GGA AAT CTT GAC AAA AAT GCC AGA TTT TCT GCC ATC TAC AGG CAA  
phe lys asp ala ser gly asn leu asp lys asn ala arg phe ser ala ile tyr arg gln

1411/471  
1441/481  
GAC AGC AAT AAG CTA TCC AAT GAT GAC ATG CTC AAG TTA CTT GCA GAC TTT CGG AAA CCT  
asp ser asn lys leu ser asn asp asp met leu lys leu leu ala asp phe arg lys pro

1471/491  
1501/501  
GAG AAG ATG GCT AAG CTC CCA GTG ATT TTA GGC AAT CTA GAC ATT ACA ATT GAT AAT GTT  
glu lys met ala lys leu pro val ile leu gly asn leu asp ile thr ile asp asn val

1531/511  
1561/521  
TCC TCA GAC TTC CCT AAT TAT GTT AAT TCA TCA TAC ATT CCC ACA AAA CAA TTT GAA ACC  
ser ser asp phe pro asn tyr val asn ser ser tyr ile pro thr lys gln phe glu thr

1591/531  
1621/541  
TGC AGT AAA ACT CCC ATC ACG TTT GAA GTG GAG GAA TTT GTG CCC TGC ATA CCA AAA CAC  
cys ser lys thr pro ile thr phe glu val glu glu phe val pro cys ile pro lys his

1651/551  
1681/561  
ACT CAG CCT TAC ACC ATC TAC ACC AAT CAC CTT TAC GTT TAT CCT AAG TAC TTG AAA TAC  
thr gln pro tyr thr ile tyr thr asn his leu tyr val tyr pro lys tyr leu lys tyr

1711/571  
1741/581  
GAC AGT CAG AAG TCT TTT GCC AAG GCT AGA AAT ATT GCG ATT TGC ATT GAA TTC AAA GAT  
asp ser gln lys ser phe ala lys ala arg asn ile ala ile cys ile glu phe lys asp

1771/591  
1801/601  
TCA GAT GAG GAA GAC TCT CAG CCC CTT AAG TGC ATT TAT GGC AGA CCT GGT GGG CCA GTT  
ser asp glu glu asp ser gln pro leu lys cys ile tyr gly arg pro gly gly pro val

1831/611  
1861/621  
TTC ACA AGA AGC GCC TTT GCT GCA GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT  
phe thr arg ser ala phe ala ala val leu his his his gln asn pro glu phe tyr asp

1891/631  
1921/641  
GAG ATT AAA ATA GAG TTG CCC ACT CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC  
glu ile lys ile glu leu pro thr gln leu his glu lys his his leu leu leu thr phe

1951/651  
1981/661  
TTC CAT GTC AGC TGT GAC AAC TCA AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA  
phe his val ser cys asp asn ser ser lys gly ser thr lys lys arg asp val val glu

2011/671  
2041/681  
ACC CAA GTT GGC TAC TCC TGG CTT CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG  
thr gln val gly tyr ser trp leu pro leu leu lys asp gly arg val val thr ser glu

2071/691  
2101/701  
CAG CAC ATC CCG GTC TCG GCG TAC CTT CCT TCG GGC CAT CTT GGC TAC CAA GAG CTT GGG  
gln his ile pro val ser ala tyr leu pro ser gly his leu gly tyr gln glu leu gly

2131/711  
2161/721  
ATG GGC AGG CAT TAT GGT CCG GAA ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA  
met gly arg his tyr gly pro glu ile lys trp val asp gly gly lys pro leu leu lys

2191/731



2221/741	2251/751
ATT TCC ACT CAT CTG GTT TCT ACA GTG TAT	ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC
ile ser thr his leu val ser thr val tyr	thr gln asp gln his leu his asn phe phe
2281/761	2311/771
CAG TAC TGT CAG AAA ACC GAA TCT GGA GCC	CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC
gln tyr cys gln lys thr glu ser gly ala	gln ala leu gly asn glu leu val lys tyr
2341/781	2371/791
CTT AAG AGT CTG CAT GCG ATG GAA GGC CAC	GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA
leu lys ser leu his ala met glu gly his	val met ile ala phe leu pro thr ile leu
2401/801	2431/811
AAC CAG CTG TTC CGA GTC CTC ACC AGA GCC	ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT
asn gln leu phe arg val leu thr arg ala	thr gln glu glu val ala val asn val thr
2461/821	2491/831
CGG GTC ATT ATT CAT GTG GTT GCC CAG TGC	CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG
arg val ile ile his val val ala gln cys	his glu glu gly leu glu ser his leu arg
2521/841	2551/851
TCA TAT GTT AAG TAC GCG TAT AAG GCT GAG	CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG
ser tyr val lys tyr ala tyr lys ala glu	pro tyr val ala ser glu tyr lys thr val
2581/861	2611/871
CAT GAA GAA CTG ACC AAA TCC ATG ACC ACG	ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC
his glu glu leu thr lys ser met thr thr	ile leu lys pro ser ala asp phe leu thr
2641/881	2671/891
AGC AAC AAA CTA CTG AGG TAC TCA TGG TTT	TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT
ser asn lys leu leu arg tyr ser trp phe	phe phe asp val leu ile lys ser met ala
2701/901	2731/911
CAG CAT TTG ATA GAG AAC TCC AAA GTT AAG	TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC
gln his leu ile glu asn ser lys val lys	leu leu arg asn gln arg phe pro ala ser
2761/921	2791/931
TAT CAT CAT GCA GCG GAA ACC GTT GTA AAT	ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT
tyr his his ala ala glu thr val val asn	met leu met pro his ile thr gln lys phe
2821/941	2851/951
GGA GAT AAT CCA GAG GCA TCT AAG AAC GCG	AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA
gly asp asn pro glu ala ser lys asn ala	asn his ser leu ala val phe ile lys arg
2881/961	2911/971
TGT TTC ACC TTC ATG GAC AGG GGC TTT GTC	TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT
cys phe thr phe met asp arg gly phe val	phe lys gln ile asn asn tyr ile ser cys
2941/981	2971/991
TTT GCT CCT GGA GAC CCA AAG ACC CTC TTT	GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG
phe ala pro gly asp pro lys thr leu phe	glu tyr lys phe glu phe leu arg val val
3001/1001	3031/1011
TGC AAC CAT GAA CAT TAT ATT CCG TTG AAC	TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT
cys asn his glu his tyr ile pro leu asn	leu pro met pro phe gly lys gly arg ile

3061/1021	3091/1031
CAA AGA TAC CAA GAC CTC CAG CTT GAC TAC	TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC
gln arg tyr gln asp leu gln leu asp tyr	ser leu thr asp glp phe cys arg asn his
3121/1041	3151/1051
TTC TTG GTG GGA CTG TTA CTG AGG GAG GTG	GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC
phe leu val gly leu leu leu arg glu val	gly thr ala leu gln glu phe arg glu val
3181/1061	3211/1071
CGT CTG ATC GCC ATC AGT GTG CTC AAG AAC	CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA
arg leu ile ala ile ser val leu lys asn	leu leu ile lys his ser phe asp asp arg
3241/1081	3271/1091
TAT GCT TCA AGG AGC CAT CAG GCA AGG ATA	GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG
tyr ala ser arg ser his gln ala arg ile	ala thr leu tyr leu pro leu phe gly leu
3301/1101	3331/1111
CTG ATT GAA AAC GTC CAG CGG ATC AAT GTG	AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG
leu ile glu asn val gln arg ile asn val	arg asp val ser pro phe pro val asn ala
3361/1121	3391/1131
GGC ATG ACC GTG AAG GAT GAA TCC CTG GCT	CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG
gly met thr val lys asp glu ser leu ala	leu pro ala val asn pro leu val thr pro
3421/1141	3451/1151
CAG AAG GGA AGC ACC CTG GAC AAC AGC CTG	CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC
gln lys gly ser thr leu asp asn ser leu	his lys asp leu leu gly ala ile ser gly
3481/1161	3511/1171
ATT GCT TCT CCA TAT ACA ACC TCA ACT CCA	AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG
ile ala ser pro tyr thr thr ser thr pro	asn ile asn ser val arg asn ala asp ser
3541/1181	3571/1191
AGA GGA TCT CTC ATA AGC ACA GAT TCG GGT	AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG
arg gly ser leu ile ser thr asp ser gly	asn ser leu pro glu arg asn ser glu lys
3601/1201	3631/1211
AGC AAT TCC CTG GAT AAG CAC CAA CAA AGT	AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT
ser asn ser leu asp lys his gln gln ser	ser thr leu gly asn ser val val arg cys
3661/1221	3691/1231
GAT AAA CTT GAC CAG TCT GAG ATT AAG AGC	CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG
asp lys leu asp gln ser glu ile lys ser	leu leu met cys phe leu tyr ile leu lys
3721/1241	3751/1251
AGC ATG TCT GAT GAT GCT TTG TTT ACA TAT	TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG
ser met ser asp asp ala leu phe thr tyr	trp asn lys ala ser thr ser glu leu met
3781/1261	3811/1271
GAT TTT TTT ACA ATA TCT GAA GTC TGC CTG	CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC
asp phe phe thr ile ser glu val cys leu	his gln phe gln tyr met gly lys arg tyr
3841/1281	3871/1291
ATA GCC AGG AAC CAG GAG GGG TTG GGA CCC	ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG
ile ala arg asn gln glu gly leu gly pro	ile val his asp arg lys ser gln thr leu

3901/1301	3931/1311
CCT GTT TCC CGT AAC AGA ACA GGA ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG	his ala arg leu gln gln leu gly ser leu
pro val ser arg asn arg thr gly met met	
3961/1321	3991/1331
GAT AAC TCT CTC ACT TTT AAC CAC AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG	gly his ser asp ala asp val leu his gln
asp asn ser leu thr phe asn his ser tyr	
4021/1341	4051/1351
CTA TTA CTT GAA GCC AAC ATT GCT ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT	val cys leu thr ala leu asp thr leu ser
ser leu leu glu ala asn ile ala thr glu	
4081/1361	4111/1371
CTA TTT ACA TTG GCG TTT AAG AAC CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG	leu ala asp his gly his asn pro leu met
phe thr leu ala phe lys asn gln leu	
4141/1381	4171/1391
AAA AAA GTT TTT GAT GTC TAC CTG TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA	leu gln lys his gln ser glu thr ala leu
lys lys val phe asp val tyr leu cys phe	
4201/1401	4231/1411
AAA AAT GTC TTC ACT GCC TTA AGG TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA	ile tyr lys phe pro ser thr phe tyr glu
lys asn val phe thr ala leu arg ser leu	
4261/1421	4291/1431
GGG AGA GCG GAC ATG TGT GCG GCT CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG	tyr glu ile leu lys cys cys asn ser lys
gly arg ala asp met cys ala ala leu cys	
4321/1441	4351/1451
CTG AGC TCC ATC AGG ACG GAG GCC TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT	leu leu tyr phe leu met arg asn asn phe
leu ser ser ile arg thr glu ala ser gln	
4381/1461	4411/1471
GAT TAC ACT GGA AAG AAG TCC TTT GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC	thr his leu gln val ile ile ser val ser
asp tyr thr thr gly lys lys ser phe val arg	
4441/1481	4471/1491
CAG CTG ATA GCA GAC GTT GTT GGC ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG ATC	glu thr arg phe gln gln ser leu ser ile
gln leu ile ala asp val val gly ile gly	
4501/1501	4531/1511
ATC AAC AAC TGT GCC AAC AGT GAC CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG	ile lys his thr ser phe ser ser asp val
ile asn asn cys ala asn ser asp arg leu	
4561/1521	4591/1531
AAG GAC TTA ACC AAA AGG ATA CGC ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT	leu met ala thr ala gln met lys glu his
lys asp leu thr lys arg ile arg thr val	
4621/1541	4651/1551
GAG AAC GAC CCA GAG ATG CTG GTG GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC	gln tyr ser leu ala lys ser tyr ala ser
glu asn asp pro glu met leu val asp leu	
4681/1561	4711/1571
ACG CCC GAG CTC AGG AAG ACG TGG CTC GAC AGC ATG GCC ARG ATC CAT GTC AAA AAT GGC	ser met ala arg ile his val lys asn gln
thr pro glu leu arg lys thr trp leu asp	

4741/1581	4771/1591
GAT CTC TCA GAG GCA GCA ATG TGC TAT GTC	CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC
asp leu ser glu ala ala met cys tyr val	his val thr ala leu val ala glu tyr leu
4801/1601	4831/1611
ACA CGG AAA GGC GTG TTT AGA CAA GGA TGC	ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC
thr arg lys gly val phe arg gln gly cys	thr ala phe arg val ile thr pro asn ile
4861/1621	4891/1631
GAC GAG GAG GCC TCC ATG ATG GAA GAC GTG	GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT
asp glu glu ala ser met met glu asp val	gly met gln asp val his phe asn glu asp
4921/1641	4951/1651
GTG CTG ATG GAG CTC CTT GAG CAG TGC GCA	GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG
val leu met glu leu leu glu gln cys ala	asp gly leu trp lys ala glu arg tyr glu
4981/1661	5011/1671
CTC ATC GCC GAC ATC TAC AAA CTT ATC ATC	CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT
leu ile ala asp ile tyr lys leu ile ile	pro ile tyr glu lys arg arg asp phe phe
5041/1681	5071/1691
GAA GAT GAA GAT GGA AAG GAG TAT ATT TAC	AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA
glu asp glu asp gly lys glu tyr ile tyr	lys glu pro lys leu thr pro leu ser glu
5101/1701	5131/1711
ATT TCT CAG AGA CTC CTT AAA CTG TAC TCG	GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG
ile ser gln arg leu leu lys leu tyr ser	asp lys phe gly ser glu asn val lys met
5161/1721	5191/1731
ATA CAG GAT TCT GGC AAG GTC AAC CCT AAG	GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG
ile gln asp ser gly lys val asn pro lys	asp leu asp ser lys tyr ala tyr ile gln
5221/1741	5251/1751
GTG ACT CAC GTC ATC CCC TTC TTT GAC GAA	AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT
val thr his val ile pro phe phe asp glu	lys glu leu gln glu arg lys thr glu phe
5281/1761	5311/1771
GAG AGA TCC CAC AAC ATC CGC CGC TTC ATG	TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG
glu arg ser his asn ile arg arg phe met	phe glu met pro phe thr gln thr gly lys
5341/1781	5371/1791
AGG CAG GGC GGG GTG GAA GAG CAG TGC AAA	CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC
arg gln gly gly val glu glu gln cys lys	arg arg thr ile leu thr ala ile his cys
5401/1801	5431/1811
TTC CCT TAT GTG AAG AAG CGC ATC CCT GTC	ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC
phe pro tyr val lys lys arg ile pro val	met tyr gln his his thr asp leu asn pro
5461/1821	5491/1831
ATC GAG GTG GCC ATT GAC GAG ATG AGT AAG	AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC
ile glu val ala ile asp glu met ser lys	lys val ala glu leu arg gln leu cys ser
5521/1841	5551/1851
TCG GCC GAG GTG GAC ATG ATC AAA CTG CAG	CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG
ser ala glu val asp met ile lys leu gln	leu lys leu gln gly ser val ser val gln

5581/1861  
GTC AAT GCT GGC CCA CTA GCA TAT GCG CGA  
val asn ala gly pro leu ala tyr ala arg

5611/1871  
GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA  
ala phe leu asp asp thr asn thr lys arg

5641/1881  
TAT CCT GAC AAT AAA GTG AAG CTG CTT AAG  
tyr pro asp asn lys val lys leu leu lys

5671/1891  
GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC  
glu val phe arg gln phe val glu ala cys

5701/1901  
GGT CAA GCC TTA GCG GTA AAC GAA CGT CTG  
gly gln ala leu ala val asn glu arg leu

5731/1911  
ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA  
ile lys glu asp gln leu glu tyr gln glu

5761/1921  
GAA ATG AAA GCC AAC TAC AGG GAA ATG GCG  
glu met lys ala asn tyr arg glu met ala

5791/1931  
AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG  
lys glu leu ser glu ile met his glu gln

5821/1941  
ATC TGC CCC CTG GAG GAG AAG ACG AGC GTC  
ile cys pro leu glu glu lys thr ser val

5851/1951  
TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC  
leu pro asn ser leu his ile phe asn ala

5881/1961  
ATC AGT GGG ACT CCA ACA AGC ACA ATG GTT  
ile ser gly thr pro thr ser thr met val

5911/1971  
CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG  
his gly met thr ser ser ser val val

5941/1981  
TGA TTA CAT CTC ATG GCC CGT GTG TGG GGA  
CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC

6001  
TTT CCA AAG CCA ATC ACT GGG GAG ACC GAG  
6061  
AAG GAA ATA AAG AAC AAC GTT ATT-TCT TAA  
6121  
CAC ATA TTT TTT TAA ATC TCA CTG GCA ATA  
6181  
TGT GGT AGA CAC TCT TGA GCT GGA CTT AGA  
6241  
ATA GAT GGC CTA CAG AAA AAA AAG GTT CTG  
6301  
CAT TGA TGC CTG GGG GAC CTT TTG CCT CGA  
6361  
TAC AGA ACT TAC TAG TTT TGT CTA GGA GTA  
6421  
TCA TTC AAC AAC ATA GAG CAA GAA TAG TGA  
6481  
CTA CTG GCT TCA AGT CAG AAC TTT GTC ATT  
6541  
ATT ACA TTT CTA CAT TTT TAA TAC TCA CAT  
6601  
ATT TGT GCT GGT CCA GTA TAT GCA ATA CAC  
6661  
GCA ATA TGG AGA TGT ATA CAA GTC TTT ACT

6031  
CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA  
6091  
CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG  
6151  
TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG  
6211  
TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA  
6271  
GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA  
6331  
CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG  
6391  
TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC  
6451  
GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG  
6511  
AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT  
6571  
GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA  
6631  
TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-2 cDNA isoforms

Isoform	Difference	Nucleotide(s)	Consequence
1	polymorphism	862	A to G change; mis-sense mutation
2	polymorphism		A to C change; mis-sense mutation changing codon from histidine to proline
3	polymorphism	2210	A to G change; mis-sense mutation changing codon from asparagine to glutamic acid
4	polymorphism	2225	C to T change; mis-sense mutation changing codon from histidine to tyrosine

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	209-291	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-2 isoforms

# human CLASP-2

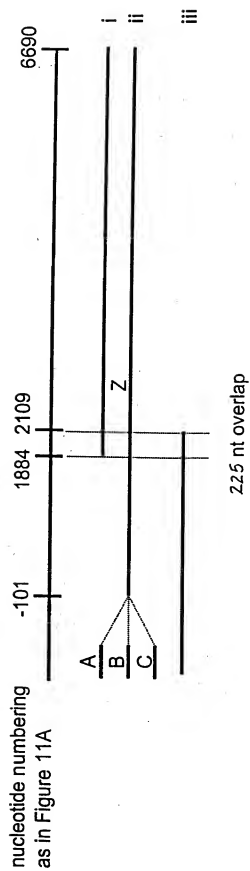


FIG. 11C

1st exon (nucleotides 335 to 445)

TGTCCTTGCTTATCTTTTCGCCCTCCAGGCCAAAGCCAAAGCTAATTGAGCCACT  
CGACTATGAAAAATGTCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGT  
TTACGGGAGATGCTGCTCTTCCCTTACGATGACTTTCAGGTAAGTAACGTTAT  
GTTTCTATCCGTAGAACCACG

2nd exon (nucleotides 7101-7190)

TTACCCAAGGCTTTTCCTCCTGTTTTGTTTCCAGACGGCCATCCTGAGACGA  
CAGGGTCGATACATATGCTCAACAGTGCCTGCGAAGGCGGAAGAGGAAGCA  
CAGAGCTTGTITGTTACAGAGGTAAGGCTCTTCTGCATTAATTTACATTT  
GAAGTCAATTTCCCCTAACTGCCTCC

3rd exon (nucleotides 11439 to 11521)

TTTTCTATTTTTAAAAATCCCCCTTCAATAGTGCATCAAAACCTATAACTCTGAC  
TGGCATCTTGTGAACTATAAATATGAAGATTACTCAGGAGAGTTTCGACAGC  
TTCCGAAGTGAGTAAGCTATATTATACACATAGGGAAAAAGTCTTT

4th exon (nucleotides 13987 to 14056)

CTAAAAACAAATTTTCTTTGTTGTTTTATAGCAAAGTGGTCAAGTTGGATAAA  
CTTCCAGTTTCATGTCTATGAAGTTGACGAGGAGGTCGACAAAGATGAGGTGG  
GATACCTGCTTGCTGTTGCTTCTCTTTTCACTCTAGATTAA

5th exon (nucleotides 15212 to 15307)

GGAGGTTGACTGCTGGTGTTTTCTTCTCTCCTAGGATGCTGCCTCCCTTGGTT  
CCCAGAAGGGTGGGATCACCAAGCATGGCTGGCTGTACAAAGGCAACATGA  
ACAGTGCCATCAGCGTGACCATGAGGGTGAGGACGCACATCACTTTGCCCTC  
CCCTCTACAAGCCCTTTC

6th exon (nucleotides 16269 to 16404)

TGAAAGAATAGCTGTGTGTATATTTTCTCTCAGTCATTTAAGAGACGATTTT  
TCCACCTGATTCACCTTGGCGATGGATCCTATAATTTGAATTTTATAAAGAT  
GAAAAGATCTCCAAAGAACCAAAAGGATCAATATTTCTGGATTCTGTATGG  
GTGTCGTTCAAGGTAAATATGAAAAGAGTTTACCATTATGTTTTCTTA

7th exon (nucleotides 19459 to 19633)

AAGTATGTCTGTTTTATCCTTTTTTTCATTTTCAGAACAAACAAAGTCAGGCGTTTT  
GCTTTTIGAGCTCAAGATGCAGGACAAAAAGTAGTTATCTCTTGGCAGCAGACA  
CTGAAGTGGAATGGAAGAATGGATCACAATTTCTAAATAAGATCCTCCAGCT  
CAACTTTGAAGCTGCAATGCAAGAAAAAGCGAAATGGCGACTTCACGAAAGT  
AGATAGGCTTGCTTCCCCCAGGCACATACACTCT

8th exon (nucleotides 20567 to 20634)



ATTACAAGTGATTCCGATAATCTGTTTTGCCATTTTAGATGATGAACAAAGCA  
AATTGGAAAGGTTCTGGTTCGGTTTAGATAGCTACCTGCCGGAACITGCCAAG  
GTAACATCGTCTTATATCTTCTGCTCTTCGTTGAATGC

9th exon (nucleotides 30257 to 30331)

GATTGTGTTAAATGTAATTTTCATGTATCTTGTATCAGAGTGCAAGAGAAGC  
AGAAATCAAACTAAAAAGTGAAAGCAGAGTCAAACTTTTTTATTTGGACCA  
GATGCCCAGGTAAGAACTATCTAAATGTTTAAATTTAAAAACCAAT

10th exon (nucleotides 31851 to 31991)

CATAACTTATTTATATGTTTACATTTTCTTTAAAGAAGCTTGACTTCTCATCA  
GCTGAGCCAGAAGTGAAGTCATTITGAAGAGAAGTTTGGAAAAAGGATCCTTG  
TCAAGTGCAATGATTTATCTTTCAATTGCAATGCTGTGTGCCGAAAAATGAA  
GAAAGACCCACTACAAATGTAATTTTTCATTTTAAAAATAAACATTAATAAA  
AAAAATAGGCAG

11th exon (nucleotides 32472 to 32675)

CCATGGTGATCATTGGATTGTTTTGTTTTGTTTCAGGTTGAACCTTTCTTTGTTA  
CTCTATCCCTGTTTGACATAAAATACAACCGGAAGATTTCTGCCGATTTCCAC  
GTAGACCTGAACCATTTCTCAGTGAGGCCAAATGCTCGCCACCACGTCCTCCGG  
CGCTGATGAATGGCAGTGGGCAGAGCCCATCTGTCTCAAGGGCATCCTTCA  
TGAAGCCGCCATGCAGTATCCGAAGCAGGTGGGGAGTATGAGCCAGCATTC  
CCACTACTCAGACTCACTTTGCATGC

12th exon (nucleotides 33063 to 33185)

GAATTCTGCTTACTGAAGAAAATGTTTGCTCTAGGGAATATTTTCAGTCA  
CTTGCTCTCATCCAGATATATTCTTGTTGCCAGAAATTGAAAAAGTCCCTCAG  
GGGAGCATCACACATTGCGCTGAGCCATATATGAAAAGTTCAGACTCTTCTA  
AGGTATGAATGGCTTTTACGCTTTGGGGTGGTAAAAAGCAATCTGAA

13th exon (nucleotides 36702 to 36784)

CAGTATCTCATAGCTTTATTCTCATGTCTTCAAGGTGGGCCAGAAAGGTGCTGA  
AGAATGCCAAGCAGGCATGCCAAAGACTAGGACAGTATAGAATGCCATTTCG  
TTGGGCAGCAAGGTAAGGAACACCTTTTATACCTTTTAAATCGATATAGATA  
GGTGCAATGG

14th partial exon (nucleotides 37353 to 37475)

GAAACCCAGTTTAGAAATGTTGCTTTGCCATTTACAGGACATTGTTTAAAGGATG  
CATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGA  
CAGCAATAAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTTCGG  
AA







13801 ACTCAAGTCTCTTGCTTACCCACCTTGAAAGCAAGGCATAGATGGTTTATTCTTGTCTGAATAAAGAGCTGGGCATCTTTGGATT  
13893 TAGTAAGGCGGGGGCCCTATGATGGAGAGAAATGCCAAGGCTCTTCTTGACTAGGCAATTCTTAAACAAATTTCTTTGTTGTTTTAT  
13985 AGCAAAAGTGGTCAAGTTGGATAAATCTTCAGTTTCATGCTATGAAGTTGACGAGGAGGTGCACAAAGATGAGGTGGGATACCTGCTTCTGCTG  
14077 TGCTTCTCTTTTCACTCTAGGATTTAAATCAATTTTACAGACTTAGAAGATTAGTTAGAAAATACCGACATTAGCCAAACAGGCATGT  
14169 GAGTGTACATGAAACGGGAATAATTTTAAATGTTATTGATTGATTGGAATAGGCTCTGTTGTTCAACTTTTACCTTGAGCATTTTCAT  
14261 GTTCTCTTGGTGTGTTTATTGTCTGAGATCATTTCAAAAGACTTGGATCAGATCTGGCTACATTTGTTAAAGATATCAAGATGACTTAG  
14353 ACTCTGAAATTTAGGTTGTTTCTTCAACAGACTCGAAACAGCTGCCAGCCAGTCAATTTAAATGGCTAATTTCTTCAATGTTCTTTAGTGA  
14445 AGCTTGATTGTATCAAGCCACTCCCTCATCTCAGAGGAAGCTCATGGCTCAATGAGACTATAAAGGGAGTAGGCGCTTGGATGAGTCT  
14537 TGGCCACTGAGTGAGGGAAGCACTCAGAGAGACAATGCCCATCTGCACTTCTCATCTCCCAATGATTGTGTAAGTTGCCATCTGTGAG  
14629 TTTAGGTTTTCTCTTTAAAAAAATGTGACCTGAGCTATACATTAAGCACTTAATGCAATGCAATGTAATTAATTTTATTT  
14721 CCCCATCACTTTATCTCTGTTCTGTATTCGCTCAATTTCTCTCTTGTCTTTATTCACCTTTCCCTGAATAGCCCTCTGGGAAGGTTTC  
14813 CAGGAATGTGCATGTGCTTTTGCTCTGACTATAGGGGAGTGCTCATTTGAAAAACATTTTTCGTGAACAGGCGAAGCCTTCCAACGTGA  
14905 GTTGTCAGTTGAGGTATGCTCTTTTGTGCTTTTGTGGCTCATTAAACACTGACAAATAAAAAATTTGGACAGGAGCTAGCTTTGCTTTAA  
14997 TGGAAATAAGTTTTCAGAAATGTAGGCGGGTCTCTCTTTCACCCGCTAAGTGGACTTTTATGTGACTTGTAGGCAATGCTGTCAATGGGTG  
15089 CTTGAGTAAGGGGCAATGGCAACTTGGCACAAGGGGAATGACCTTCCATTGACCAAACTCACAGCAAGCAACCCAGGTATTAAGCGGAG  
15181 GTTGAGTCTGGTGTCTTCTCTCTCTAGAGTGCTGCTCTCTCTGGTCCAGAGAGTGGGATACCAGAGCACTGGCTGGCTGTACAAAG  
15273 GCAACATGAACAGTCCCATCAGCTGACATGAGGGTGAGGACGCACATCACTTTGCGCTCCCTCTCAACAGCCCTTCTGCCATAGAGCT  
15365 CGAGAACATCTCTCAGATGAATGCGCATGCTGTTCTTCCCAACAAAAGGACATTTGCTGATTCCTAGGATCTCCCTGGTGATAGCACC  
15457 CCCATTGGCAGCGCTCATCACCACCTTTCCCTCAGCTGCTCTGACCAACAGCATAGGAGCACTCCCTGGCGGTGTGAAGTGCGAG  
15549 ACACGTGACATAGGCTTTCTTCTCTGTAATACGTAAAGTGCTCTTTGTGACTCTACAGATGTCACCAAGGGGCTATCTGTCTATGCCAAT  
15641 CTGAGCACTTCTGTGGAGGTGTACTGACGCAAGTCAAGTAAGCAAAAAATTTGAGGACGAGAAAGAAATGTGCTATAGAGAGAGAGGTT  
15733 CTGACAGAGAGTCAAACTAATAGAGAGCTTCTCAGGAGAAAGTGGGACGAGGAACATCAGGATTAATAACAAAGGGAAGAGAAAC  
15825 AAGGGAGTCAGGGAGATAAAATTAAGGAGAAATGTGACTGTCAATACCTAAGGCTGAAAATCTCTCAGCTCATGAGGCAAAAATAG  
15917 TTCCCATCTGTGACAGAAACCCTCGGGGATTTAGAGAAAGTTTCTGTCTCTGCTGATGCTATGCCAATTTGGAATTTGCAATCTGCTT  
16009 TTGGGTAGTTATGTAAATCTCTGATTCCTGGTGGTGAGAAAAATGACCATGGATATTAGGGGAACCCACTCTCTCAGAATGAGATGCAATG  
16101 AGCTCTTAGATGGGATGGGAGCTTGACCCCAAGTGCACCTGGAGCATCAGCTAGAGTGAGAACGGAACAGGTTTATGTATGTATGTA  
16193 GTCATAGTGGGTATGTATGATAGAGTTGTGACCTCTTCAATTTGAAAGATAGCTGTGTGTATATTTTCTCTCAGTCATTTAAGAGCGGA  
16285 TTTTTCACCTGATTCACTTGGCGATGGATCCTATAATTTGAATTTTATAAAGATGAAAGATCTCCAAGAACCAAAAGGATCAATATT  
16377 TCTGGAATCTGATGGGTGTGCTTCAGGTAAATATGAAAAGAGTTTACCAATTATGTTTCTTATCTGCAATAGTGCTTATGTGTAATTA  
16469 GCGAGTTTAAGCAACACTTCCAAAATGGCAATATGCATGGTAGAAATATAACATATAAGCTTTAAATAGGCAAGCCCTGTGTTTTCATCAT  
16561 TGTAGAGATGGAAGGATAATGTAGAGGCGAGATTATGCTGTGGCAGGCGAGGACACTCTGCTCGGCCACTTTATAGCTGCTGACCTTT  
16653 AACAGGCTACTTAATTCAGATAATGAGATGTTTCTTTAATACGGCAATAGTACATTTGAGTGAATCAGTGCAGGAAAATATTAAAAAC  
16745 TCTCATGTATCTCAGTGGTGATTTTATCTCGTAGCATGTAGTACCAGTGGCGGTGTAGATCAGTAAAGAGATTAGGTTTACGCGCAATG  
16837 AGTTCAATCCCTGCTCTCCCTCACTACCACTGTGTAACTTGGAGATGTATTAACTCTCTGTACCTCAGTTTCTTCAITTTGTTAAAT  
16929 AGGATAATGGCAGTACCAATATGGTTACTGAGAGGGTTCATTCATTACACATGAAAAGCTTAGAACAGTGCACCAAAATGTTAGCAAT  
17021 TGCTCAGTATAGATAGTTTGTGTATCATAGGGGCTGTGTACTTTTATATCATAGGCGTTATGTACTTATGCTTTTAAAAATTTATGTTAATTA  
17113 AAGATAACCATGATGATATTTTCTGTGAAGAAATCAGGCAATACAGATAAAGTGAAGGCTCTCTGGAATCTCCCTCTCTCAGTGCT  
17205 CTTTCTGAGGGGAGCTACTACCAATTTGCATGATCTCTGTGACCTTTTAGCAITTTTAGCAITTTCTTTGAGAGTGTGCAATTTCCCTGTGCC  
17297 ATCATCTGTCATCCATCATCACTCATCCATCTGTGCCCCCTCCATTCATCCAGCCTTGCCACTTTCAAGGAAGTTTAAAGCAGCAGC  
17389 TTATPAGCATACACAGGACATGGGATAGCATTAATTTAAAGTGGGGGTGAAGAGCAAAAGATGAACAGGGGATTGGATTAAGGGTGAGAGAA  
17481 AATAGATTAAAGGAGAGCGGTATTTTGAAGATCTAACACTGCTGTGGGCGGACCACTCTGCTGCTTCTCAGTTGAGATTTTCCCTGAGAC  
17573 CTGTTTAGTCACGCAATTCACAGTGCACATGAGATAAAGGCATGATGCTGTGTTAGTGCACTTAGAAGCACCCCTGACTTTAAAAAGAGT  
17665 TAAAGCAAACTAAATGTTATTGGCAACCTCAATTTTAAAGTAGGAAGTAATTTTGTGTTTATAAGAGAGTTTTCCTGCTGTTTCTG  
17755 GCGCCAGGACAGATGTTTATAAGTCAACCTGCTGAGCTATCAATTAGCTCTCGGGGTCGATTTCAAAATTTAGAACCTTGAATTTTCAATGG  
17849 AAGTCTCTCTTCAATTTGCTTTGAGATGCAGCTGATGGTGTTCATTATTAATAGGTGATCCAGGCTTCAAAAAGTAAATTAAT  
17941 TGTTTATGCTGTGCTGTTGTGAATAAGCATCAAAAGTTGTGATTAAAGTGTTTAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT  
18033 TAGTTGACTGGTCTGTGAATTAAGAAAAAGTGCCTAACTAAAAATTTGAAGATTTTAGAACCTTGAATTTTAATTAATTAATTTATTTG  
18125 AGATGAGAAATCTGAGGCTCGAAGACAGAAATTAAGAATTGAGGCTAAGTGTGTTTCTTCCATTTTAACCTTCTCTTTTCAATGATTTGA  
18217 GTATGACGGGAAGGAGGAGAAAAATCAATTTTGTCAAGCCTTTGAGCTTCTCTGCTTGTGCTGAGTTTAAAGTGAATGCAATGGA  
18309 GTGCGCAATTACTGAGGCCACAGCAGACATCTGTGCACAGAGATGTGTGCTTTGCCAAGGGAGCACTTGACTTTGCATTTCAAGACTG

18401 TGCTGCAGAAATCAGACAGACTTTTGGGAGGGTGGCCCTGTCCCTGAGACCTCCACCAAGGAACCTCTAGAGAGAGTGTGGATTAACCCAGTAG  
18493 GATTTTAACTGGGTATGGGGGGCTGTCTCTGGCTCAGGTGTAGTGGGAGTGTGTAATTCATATCGCTCAGCGCTGTCTTACAGGGGATC  
18585 TTGTGCCATGATCTCTCAGAGCTGAACCTCTGTCTACTGCGGCCAACCTGGGAGATTTTGTCTCCCTGGAGGACATCTTGGAAATGTCTGAAGA  
18677 CTGGCATCTATTGGCTTAAGGCCATAAATTTCTGCTAAACATGTGACAAATGATGACAGCAGCCTCACACAAGAAATATGGCTGCCCAAGT  
18769 TCAGTAGTCCAGGATTAAGAAATCTGGCCCTAGTGCATGTTCACTCTCCGTCTGTATGTCACATGACAGTCACTGTCTCTTCTGTCTGGCC  
18861 AGTCACCTCTCTGACGGCATGAAACTGGAGGCATGAGCGAAGCCACGGACAGGAGTCCAAATACCTTTTGGGATTCATAAAGATGGGA  
18953 AAGTGTCCAGATAAGTAAGGCCAATCATAGTAAATAGATAATGGTTGGCTTTTAAAAATGTAAATACCATACACTACTCTTCAATAAAAAATAGGAG  
19045 CTGAAGAATAATGAAATTTTACATGAATTTTCACTTATTCACCAAAATATTTTTCAAATCCCACTATGTGCAAGTCACTGTAGAGTCCATA  
19137 GAGACTAAGGATGTGTAGCACTGACAAAAATGGCAGCACTGAGGAGGTTTCAITCCACTGCAGGGACACACAGTGAATCAGATGAGTATGTA  
19229 AAGCAGGTAAATGAGTCAGAAGGAAAAATAAGCTTCGACAAAGTGAAGCAGGGAAGGTGGACGGTAATGGGATTTTCAATGGGGGGGGCTTTC  
19321 ATGAGGAGGGGGCAAGCTATTATAAATAGCTTGGTTCTAAATGCCAATGAGATCACTACCAACAAGAGAGATTAATATTTTAAAGCAG  
19413 TTCTAATTTCTTTAAAGTATGTCTGTTTATCTTTTTCATTTTCAGAACCAAAAGTCAGCGGTTTGTCTTTGAGCTCAAGTGCAGGACA  
19505 AAAGTAGTTATCTCTTGGCAGCAGCAGCTGCAAGTGGAAATGGAAGAATGGATCACAATTTCTAAATAGATCTCTCCAGCTCAACTTGTAAAGCT  
19597 GCAATTCAGAAAAAGCGAAATGGCGACTCAAGTGGAGTATAGAGCTTGGCTTCCCGCAAGCATACACACTGTGGGTGTCTTTATTTT  
19689 TGTCAGGTGGGATAAAGAGGAGACCTGTGTATACACAGTACATGAGAGGTGGGACGATAGGAGGCTTTTACAAATATCTCTGCAGCAAA  
19781 GGTGTTGTCACTTAATACTTCACTTCCCTGAGCAATTCGTATATGGAATCATGTAATGGGAACCAAAAGCTTTTGGAGCGAAGGGAGA  
19873 CCTGGGTTTGGTGGCATAAATACTGTATTTACGCTGTGTAGGCCCTGGGTAAMCAACTATGTTTCTGAGCCTCAGTTGACTCAGCTATAAA  
19965 AATGGGATAAATCAATGAAATTTCTGGGAAGTGGGAAGTGTAAATAAGAAATGAATCTCAAGTATCTGGCATAGATTTTACTGTATAT  
20057 AAATATTAGTAATTAATTAAGTGGTGGAGGCTCAGATTAATTTGGTAGAAAAATCTGGCTAATGTTCTGCAATTCAGTTTACTTCTC  
20149 AACCTTAGTGATTTCCCAACCTGGCTTCCCTTAGAAGTACCTGGGAGCTTTTAAAAATACCAATTTACCTGGTCCCAAAAGATCTCG  
20241 ATTTAGTTGGTCTGGGCTGGAGCTGGGCAAGTCTGACTTTTAGGGGGTCTCATGAGCAGTGTCTCATGTGGGCTGTGTGTCTATGAGTAGTGTC  
20333 AGTCTAAATGGACGGTGTCCATGCTATACAGCTCAGTGTGTTGACTTTTATCAGTACAGGCTGTGGATCAGTATTTTTCAAAGCAAC  
20425 CCAAGTGTCTCCAGGAGCATCCAGATGGGGAGCACTGTGTCTTATGAGGCACTAAGAGAAAGGGGCTTCTCTCTCTGTTCATAT  
20517 GAAATGATTAATGAATTAAGTGTCCGATAATCTGTTTGTCCATTTTAGATGATGAACAAAGCAATTTGGAAGGTTCTGGTTCGGGTTTAT  
20609 ATAGTACTCTCCGGAATCTGCGAAGTAATCACTGCTCTATATCTCTGCTCTGTGTGAAGTGTGTGAAGATGTCTCATTTACTGCTTACTGCT  
20701 TGTCCAGAATGGAATCTGTTGAATCATAAAAATACATTTGTGATTAACCTCTCTCTTTTCTGACTGATTAGCAGGTGACGTGTACTCATG  
20793 CAGTATGATTTAGGCTGTCTCTTAAAAAGTACCTACAAAGCAATCTCTCTTTTATTATTTTAAAGTGTTTTTCCTGTGAATGCTT  
20885 AACACTGCATCAGAGTACTGAGAAGTAATCACTGAAATATGCAGGCAGATGTCTCATATAGCATCGTACTTTCTATGTTGATACATGTGCT  
20977 CTCCCTTACTCAGGCTAATAGACACGGTCCAAAGAGGAGGAGCTGGTAATCTTGCCACGAAGCCGGGGGTGCTCGAGTACAGAAAAAT  
21069 GTTTCGGGTCACTCTTACTGGAAAAAATAAGCAITTCCTGTGTCTTACAATTTAGAGAAATTTAAAGTACTGAAAGACCAAGGAAA  
21161 GCAAAATCAACATACTGCTACTTCCAGATTAATAATCTATTATGATGTTGCCCTTTTAGCTTCCATATTTCTAAAAAGATAAATAACATGG  
21253 TATAGTTGAAGTCTTTTAAAACTGTCTCTTATTCCTATCTCTTCTCCCAACACCCCAATCAGAAACAGCACTATTAAAAAGTTT  
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21437 TACCATATGATTTCTGCACCTTTAAAAAATTTTAAATTTACCCCTTTTATTGTACTATATAGACTTTTATTTAGCTGTCTATATTTT  
21529 CATTTTCTTTATTAATAAAGCTACATGACTGCTCTTGTACTTGTGCTGTGTGTGTATCTGAATGATCTTTCTTAAATGAGGAGAAA  
21621 TATCTTGTCTCTTCTAGCCCTCTTGCACCTTACTCTGTACTGCTCTTCTATTTCTTTGTACTGACTGAGGAGAAATGGCAGCTCCACAC  
21713 CCACATCTTAAACACTATAATAGAAACATGTTTATCTATATAGGATTAATAATAGACAGCACTCAGCACTTACCTTTATTTAAGACAC  
21805 ATGGCTGTCTCAAGTGTAAAAATCTCCCTCCCTGGCTAGGGCTTTAGAGCAATGTGTTTCTTTAGGACTTGTACTGCTACACAGATCTTTT  
21897 TAGCCTCTGCTATTAAAGCTTAATTTTGGGCTCAATGTTGAGCTGCACCAATGTAAACCACTCTAGTCTGGGAAGATTTGGCTGTGTGTTGTGTAT  
21989 ATGCTGTGTATCATATTTTGCATTGAGATTTGCTTTTGTGTTCTGGATGTTTGGGGGTCTATAATTTCTCAAAAACAAATATTTGTGCGCC  
22081 ATTCTGGGTTTAGTTTGTGTCAGCAGGTAAATATGTGATGCCATCTAGAATTACAGAAATGAACTCTGCACTTACTGGGTGAAGCGAATG  
22173 GATTCATAGGAGAAGATTCATGTATTTTGGGCTCAATGTTGATTAATAAATACTGCTTTTCTTATGAGGATATACAGGAAAGCGTCCCT  
22265 CTCTCTCTCTATACCAGCAGCAATAATATAGTATGTTTGTATCCCAAGCACTAGGAGAGATTTTAAAGATATACATATTTAATATAT  
22357 ATGATACATTTATGATATACATTTTATTAAGATAATGTGTATTTTGTCAATTTAAAAATTTTAAACTATTTTAACTATGGGTTA  
22449 CAAGTTAGGTTAAGCAATTTAGTTGGTGAATCAGTTTGAATTCACCCCTGCTTCTTTTGTGTTTGTGTTCTATTTAGTTTATTTCTTT  
22541 TTTATGAGGTATATTTTGAATAGCAGATGCTCAAAACATGAATTTGAGAGTCTGAGTCTGAGTCTGTACACTGATATAGCAGCCCT  
22633 CAGGCTAGCTGTACTGAGACCTCTTTATTTTGAACCTCCATCAGCTGATAGTATGTTTGTACTTTTCTAGACCTTCTGTGAATGGACTTA  
22725 TACATGACTCTTTGTGTCAGGCTTATTTAGCTAAACATGTGATCTACCTTAAGAAGTTTTTTTAGTCTGGGCATAGTGGCTCATGCCGTG  
22817 AATCCGAGCACTTTGGGAGGCTGAGGTGAGCGGATCTTTTGAAGTTAGAGGATCAAGACAGCCTTGCCACAGATGATATAAACCTGTCTC  
22909 TACTAGAATAACAAAATTAGTACGGCTGTGGCAGGTGCTGTAACTCCAGCTACTTTGGGAGGCTGAGCAGGAGATCACTGACTG

FIG. 12B  
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23001 GAAGGCAGAGATTGCGAGTGAAGTATGAGTACCTGACCTGAGCTGGGTGACAGAGCAAGACTGTGTCTCAAAAAAAAAAAGGGTC  
 23093 CGTTTAAATGAATAAAATGGAATGGAGATATGAAAGTACACTGCCCTTAATAATGACATTATTTTTATATAAAATACTGTCATTATTA  
 23185 TTTGGTGACACTGCCACCACTGCTAGCTAATTTTTGTATTTCTAGTAGAGACAGGGTTTTATACCATGTTGGCGAGGCTGGCTTGAACTC  
 23277 CTAACTCTCAAAGATCCACCACCTGAGCTCCCAAAGTCTGAGATTACAGGCATGAGCCACTACGCCCGACCTGAAAAAAACTTTTTAA  
 23369 AGTGAATTAACATAATTTTTACATAAAATATGTCATTATTAAGGCCAATGTACTATTTATACATATAGTGTGTATGTGTGCTTCATATG  
 23461 GATATAAAGATATTTTGTTCCTTAGTGCTATTTATGTATATTTATTTACTTGGTATATAAGTGACCTATTTTGGGATGCTCATGT  
 23553 GATACTTTGATATCTGTATCAATGTGTGATGATCAATCAGGATAATGGGATAGCCATCACTCAAAACATTTATCTTTTGTGTGGGAATT  
 23645 TGAACATCTTTCTTACCGAGGCTCATGCTCAAACTCGAAAAATGAATCTTGTAGAGGCTTTTACTTTCCCTCGCTTTCAGGTGTTT  
 23737 TCAAAATCTTTTATTTAGGAAGGTGAAGAGGTGGAAAGTAATTTTTGAAGGGAAGAAGATGAGAAAAATGGAGATGAGTTATTTACTCA  
 23829 GCACATGGGTATCTGTGGGCTTTGCCCTTTTAAAGGCCAGCTTGGTGTGAGTGTGACAGCCAGCCAGGAGTAAAGGGGAGACCTGTGTTCCCAT  
 23921 CCGACCTTTGACCAAAATACGATTTTTGGCTTTATCATCCCCCTTCAGGCTGTCTAGATTTTGCACCCGTTGAGAAGGCAAGAAT  
 24013 TGACCTGATAACTGTTGGTCACTCCATTAGGAAGGATGGATTCATGGTTACAGAAATCAGAGACTGAAGTATCGAGAGGGAGGGGTGGGAG  
 24105 AGAGACTGTGCAAGGAGTTTACCAGGGTATGAGAGGTAAAGAGGTGAGTATCAGGGAAGGAGGTGCAAGAAAGGCTCAGGCTGGGAG  
 24197 CTGGCCACAGTTCAGTAAGATTACAAGAAAGGGCTAGAACATGAGGGCAGGCAGAGGTGGCTGAAGGTGTAATTTTCATGGCAGGTCTC  
 24289 TTTTCTAATCAGCTCCTCTAACCTCCTTCATCCTGTGCCCCGGCTTTTGTCTTCCACTGTGACTAAGACATAGCCAAACAGGATATGACCG  
 24381 ACAGGAAGTGTGTTTCAGTGCAGAAAATACTGATGCTCATCTTGGAAATATTAGGAAGGCTCTATTACATGAGTGTGATGTAAACCC  
 24473 AGGTTTTCAGATAATTTGTATAATCTTGGAGCTTGTGTTGTACATTTAGTACTGAACCTCATGTTGTTCTTTCTATTAGAGAACACTGT  
 24565 TATTTACCTCAAACCTGGTCTTTCTCTCTCATTTGCTATTTATGGAACCAACATTTTTATGTAAATGACACAGTGTGTAGCATCAGTCT  
 24657 TATAAATATTTAGTTTGATACACAAACCGTAGTTCAAGTTAGTTAATGATTTCTTCCCTAGAAAGTCAAGGAGTAAACATATCAGGTTAT  
 24749 AAACCTCATTACTAGTTATTTAATAATTTATTTCTCTGTTACATTTATPATCTCTAGGTGACATCAGAACATATATGCTACCTCTTAAAGT  
 24841 AGTGTGAAGAAACCCACCTATGTTTCTTCCACAGCTTTCTGTTTGTGAGCTTTATTTTGTACTCAAGAGATAGTCACTCAACTTTTAA  
 24933 TCTTGGTCTTCCCATGTGGTCTGAAAGAGAAGTGAATTTCTCTAAATCCGGAATGTGTCACATCTTTTACCTTTTAACTTGTGTTAA  
 25025 GCAATGAACCTTATGTTGCTGATTTCTTCCACAGTGTGCTCAGGGGAAGTATGATCTCTCAGACCTTTATAGTCTCATGGAGATGGAG  
 25117 TGAGGATCAAGGCGTACCTCAGCAGAACTGTGAGGACCCAGCAGTTTCAAGGCAACCTTTTCTAAATTTTAAACCAAGTCTATAATAG  
 25209 TGGTTCTCTCCATGTTCCAACTCAGAAACAAATCATCTATATACAGTATATACAAAGAGCTGCTGAGCTTGTGCTGTGGGCTCAGCTGG  
 25301 TGCTGCATTCTCGGGCTCCTTTGTGAGAGGATGAATGATGCTCCTGGAAGTTAGGTGCTTGGAAAGTGGAAATAAATCATGATAA  
 25393 CTCCTTAAATTAAGAGTATATATTTTGGCTCCTAAACATTTTGCAGAGCTCCTCTATOCACCAATCTGTTTAAATGCCCAACATCTCA  
 25485 ACACATCTGTTCTGATAAATTCATCTCAGAATAAGATGCTGTTGGCCATACTTTGCTCTAGATTGTTTATCATCTGCCAAATAATTT  
 25577 AAGACACAGAGTATGCTTAAAGCTACAGCAGACTTTCTGGAACCTCTGAATGTTGTGCTCATAACTACTTCTTAAGCAAGAAGAGAAAC  
 25669 CTTGCTCAGGCTGTGCTATTGCTGTGAATGTAGGTTTACAGGATGGGCTGGGCTGGGGAATCGCCCTTGGTTTAGATGAATCATCTTCT  
 25761 TCCTTGTCTCTCAGGAAACACAGTTTCTCAGAGAAACAGCTGTGCAITGTGCAATTTCTGCTCCATTTCTCTCAITCTCCTCTCA  
 25853 CGAAACCCAGAGTAGTCAGTGGGCTTTGGCGAGAAAGTGGCAACAGGCTGTCTGGGGAAGGCAGTTGGCTCTTTACCATCACAATAT  
 25945 AGACTGACCAAGCGTTATTTAAGAGCAGAGCTGGTTTCATCAGCTCTGAGAAGTGTCTCAACTACAGACTTTGGGATGATATTTGTTATAGC  
 26037 TGTATTTCTTCCAGCTCTAGATTGTGAAGATTTTCTGATACATTAATAATATTTATTTATTTACTTACAAAAATTTAATAAAGAGGGTGTCT  
 26129 TGCCGCAATAGTAAAAATACCAAGTGTGTTAAGAAAGTTCACCTTTTCCCTTATCTCTCAITTCACCATCTCGACACACTGAAG  
 26221 TTAATAACCGGTTGCAATTTCCCTTTCCACAACTGATGCTCATAGAAATATAGTAAACATCTACAGATTTTAACTTTTAAATAA  
 26313 AATATGTCATGATATACATTATTTGTAATTTTCTGATACATTAATAATATTTCTATAGTGTCCCTCTGGGCCAGTGAAGATCTGTT  
 26405 TCCCCCTACATACATATCAGCAAGCTGCATGATATTTCACTATTGCTACTGACAGATTATTCAGCCATCTCCCTATTATGACATTTTA  
 26497 AGGTTTTTTTTTCAGTTTTTAGCTCTACAAAGCTACACAAATAACAACTGACATTAATATTTTGTGCTCTTATTTCTAGGAGAAAT  
 26589 CCCAATGTGGAATTTTTAAGTCAAAGTTATTTGTGTTTTAATGCTTTTAAACATTGCCAGGTTACCGCTCCAAAAGGCTATAACAATTCAC  
 26681 ATTTCTGTTCTCTGCATCTTCACAGAGAGGTGTAATGATGTTATTTACTGCTTTCAITTTATATTTGCTGGTTATTAGTGATATTTT  
 26773 CATGTTTCTATATATTTTGTGCTATTTGTTGTTTTCTTCTGACTGCTGTGTCAGATTTTACTGTGTTTCTTCTGCTGTGTGATG  
 26865 GTAATAGTTTAGACTCTGAAGCCAGGCACCTGAGTTAGAAGCCAGGCTCTATTTCTATGATGTAGTCTTTGGGCAAGTACTTAACATTC  
 26957 ATGCGCTTAGTGTGTTTTCTTTTAAATGAGCAGGATATAATAGTACCTGCTCTCAAGGTGTATAAAATTAATAATGGGCATTAGGCTAAT  
 27049 ATCTACAGGCTAGATATGGCTATATCAATAGTACCTCTTACGTTACTATTTCCAGATGTTTCTCTGACTCTGGGCAAGGCTCCTG  
 27141 CTACCCCTGAACCACTATTTTCTACCTCTTAGATTACTTGTGTAATGCAATCAGCCACTGTTGGGCACTCTCTGTGTTTATGTCATCATCT  
 27233 TAGACCTTAGAGGGATGGGAGAACCTTTAAGAGCCGGAATTTGCTTTTATTTATCTTGTAGCAGACATAGATGATATAGGTAGATT  
 27325 ACAAGCTTTTAGGTTATTTTGTCACTAAAGCTGTCCCTCTTTTCAATAAATGATGTCTGGTGAAGAATATATCTGTGGGTTGTAGT  
 27417 GACAAAATCAGAAATGCTTTGTGCTATTTTGGCTAGTAGTTAATGTTTTCTTTATTTGTGTGCTGATTCCTATTTGTCTTTAATATAC  
 27509 CGAGCTCATTAGCAGTTATTTCTGCTTTATTCATTTCTTATCTCTAGCATAGTCAGCTCAAGCAACAAGCATCTTTCAGAAAGCCACTAG





32201 GACAGAGTTCATCTTAGATGCTTCAGGGAACGCAACTGTGTTTCATGGAACATACATTACGTAGCAAAACACATAAAGGTAAAAATATG  
32293 TTTTGTGTTGTTCTCTAAATTTGTTTATAGCTAATTTCTCTGTATGCAGAGGATGAGACTGTTTAGTAGTAATTTATGGCAACAGCTCTAAA  
32385 TAGGCTCTGTGCTATTTCTCTTTGTATGACCAACTCTTTTGCCCTGTTTGAGCCATGGTGATCTGGATGTTTGTGTTGTCAGGTGA  
32477 ACCTTTCTTTGTTACTCTATTCCTTTTGACATAAAATACAACCGGAAGTTTCTGCGAATTCACGTAGACCTGAACCATTTCTCAGTGA  
32569 GGCAAATGCTCGCCACCACTGCTCCCGGCGCTGATGATGTCAGTGGGCAAGGCCATCTGTCCTCAAGGGCATCTCTCATGAAGCGCCGAT  
32661 CAGATCCGGAAGCAGTGGGAGTATGAGCCAGCACTCCCACTCTCAGACTGATCTTGACATGCTACCTAAATGCACCAAAATGCTCAA  
32753 TTAGACCTTGTAATGCACAAGTGGGCTCAATAGACTCTTAATTAAGTAGTATTTATATACAGTAAGAGGCTGAGAAAATAGTGCTC  
32845 TTTAATGCTCTTTCTCTTTCTTAAAGATTTCTCTAGTACCTCCTCACCATAAGACTTTTTCAGCAGAGATGACTGTTTGTGTCAGCTAA  
32937 CTAGTTTGGCAGTGGGCTTTTCTACTAGTTGCTCTGTTTCAGTGTCTTTGCTGTAAATGTTCTCATGGGATTTGATTAAGTAGCTGTGA  
33029 TTCTGCTTACTGAAGAAAATGTTTGCCCTCTAGGGAATATTTTCAGTCACTTGTCTCTATCCAGATATATTTCTTGCGCCAGAAATGAAA  
33121 AAGTCCTTCAGGGAGCATCACACATTCGCGCTGAGCCATATATGAAAGTTTCAGACTCTTCTAAGGATGAATGGCTTTTACGCTTTGGGCT  
33213 GGTAAAAGCAATCTGAAAGAGGCCCTTATGTGATACTATAAATCTTAAATGAATCAACATAGCCATATTTATCTATAAAGATGTA  
33305 GAATATGCTACTGTATTTACTCTGAACCTTATGCTCTGATTTGAAAGAAATGTAGTCTATGTGTAATAAATGATCCACTTGACTAGA  
33397 CAGTTCTGCATCTCTAAATAATTTGCAAGGAATTACAGCTTAATAGTAAATCTTCTGTGTAGAAGGTACATGTATGATTTCAAAATG  
33489 AGTTTCTCTAATCTGTAATTTGCTCTTGGGTTCTGAATCTTAITTTGGTCCACTTACATATATATAGAGCTGGAGACAGGAGATGC  
33581 CCTTGGCTCAGTAGACTGGCCAGCAGTGCAGTAGATTACAGTCCACTTGGTTTTCCTAGAAGGGCAGAGTTTGTAGTGGAGATGGAAA  
33673 GAAAACATACATGATGTATGTTGGTTTTTCTTCAAAGTAGTGTTCACTATGGGAAGTGCCTAGGCAATGCCATACCATGTAATTTAAAA  
33765 TATTAGAGTCACTAGTCAAGATGCTCTTCAATTTCCAGGACCTGAGGCTCACCAGGCTTAGTGATCTGCTCAGTGTCTCATAGGCTG  
33857 GAGCTGCCAGGGGCACTTGAACCTGCCACTCTGAGCACTTGTGCTACTGGTATGTAATCTGTGAAGTCTATATCTCTGCGCAATTCAT  
33949 ACATATTTTAGTATTTTAAACAAAATTTGTGTGCTCATCTGAGAGGCTGTAATCACTGACAGGAGCTGTCAGCAGTAGGAGTGGATG  
34041 CCCAGAGTGTGAGTGAAGTTTACTAAGTTGGATTGAGGCTTCTATCTTCACTCTTATGGGCGCCCATGCGATCAGAGCTGTGTCACAG  
34133 GATGCAGATGGCATTGAGAAATGGATTTTGGAGTCAGAGACCTGGGCTGCGATGCTTAACTCATCTGGGCTCTTTGGACAGAAATCACAT  
34225 CACTCTCATGGCTCCATATGTTCTTCTGCGATGAAGGATGATGTACTTCTTGCTCTGCCITCTCATAGGGACAGTGTATAGATCA  
34317 AACAGATCATGTATGAGTCAGTGCTGTGGGCCACCATAAATCACAGAAAGCCAGAGACATGTCATTATTACAGCCCAGTCAAGTAAAA  
34409 GCCCAATTACCCAGGCACTTGGTTCCACAGTAGAGGCTTTTGGCTGATGAAAGCTGTGTAAGTTTGTGCTCTGGAGAGAGGCTGTTTAA  
34501 TTTTAAAAACAGACTGTGAATAACCTTGGATGAAGACTCTTTAGCTCTTTTATGTTTGTATCAATATCAATGAAGGCCCAATATAAGA  
34593 TCTCTCCCCCGACCGTGTATGCAACACATTTCCAGGGCCATCCACAGCAACTTGTGTACTTCTGCTGCCGCATGCTGTTTGAATTT  
34685 GGCAGCTCATATGGTGTAAAAATCACATATCACTGTAGGCTAAACTTACCTCTGCACACTCTCTTCGTGCCACTGAGCATCTGCTGAAGTC  
34777 TGCCTTTTCTCATTTTTTTTGAAGATGTAAAGCTCATCCATGTGTACATTTATCATGCAATTAATCTTCTGCGCACTCCAAAGCATTCAT  
34869 TAAAGCAGGAATTAAGGCTCAACTATCTTACTTTAGCACTGTTTGGCAGAGATGTACAGTGAGATGATTTTTCTGTCTGTCAAAGTTG  
34961 TTTCTCATGTTTTCCAGATGGCTAGAACATCATTTAGAGTAAATTTTCATTTGGAGGAAATTTTATGAAAAGTCTCTGTAGGTATCT  
35053 CCTGTGATAGAGGTTTTAAAAAGAAAAGAGGGA AAAAGGCCAAAGGAAAATAAGTTTCTTACTCTGACTTTTACACATCTGTG  
35145 TTCTAATTTGCTCTCTTATATGCTGAGAGCTAAGTCTCATTCACTCGAGAAAAGGCTTATGATGTTTATGTTTGTAGCTTTAACTTTTA  
35237 TGAATATGCTCATTTTTTACTCCACACATATTCATCTTGTAGAACAAAAATCTGAACTGAAAATGTTTAAAGATTTGACCTGCA  
35329 GCTAGGTAGGCCATTGTACCTATAACTCATACACCTAAGACCCCACTAAGTGCGCCACCCAGGAGGAGCAACATACCTCATTTGAGAA  
35421 GGGGGAGGCTGTAGATGATCTCTGACATCTCTTCAATTAGGATGATATTTTCAGGATCATCATGAGGACAGCAGTCTCTACAGCATAT  
35513 TATGTTAGGATTATAAGTTTGTCACTGAAGAGGATCATGAAAAGTATAGCTCAGGCCCACTTTTCAGTGTGATGATGGAGCTCAGAGA  
35605 GGTTTGATGGCTACAGAGTCATACAGCTGGATTCAGTGTGACTTAGAGACAGACAGCTCTGTATCTAGATCTCTTGGATCTCTTAGAT  
35697 CCTCTCTGTGCTGATGTCACACAGATCACCGAGGCTCTGTGCAAGACGCATCTCTGATCAGAAAGTTTGGGGCAGGCTGAGACTC  
35789 TGTCTTCTCAGTGAATGTGATGCTATAGCACACTTTGGTTTGGAGTACATTTCCAAAATGGTTTGTACTTTGATTTAGTATCTATATAA  
35881 GACCTCTCAGTAAAAA AAAAAAAAAAATTAAGTAAATGTAAGAGCCCTTCACTGTAACTCTGAGACAATCAAACCTTGCAATGATGACA  
35973 AGGCACTATCAGAGTACAGACAAATTTGGA AAAATTAAGCATTATCTTTTATGCAATAGGGGTATAGATGATTAATAATAGGCTTGCTCT  
36065 GGC TAAAGCAATTAAGCTTCAATGTACACTGTGAATTAATCAATCAATCAACACAAACAAATTAAGCTATGAGAGTANAATAGCAG  
36157 TAAATCATGTTTAGAAGCAAGATATAGCATGTGAAGACCCAGCCTAACTGAAGTCAGTATCTTAATATCTTATCCCTTATATTGTTGGGA  
36249 TCAGCATAAAGCTAGTGGCTTTAGGAGCTGTGAAGCTTAGTATTTTAATAGTGTCTCATTCAATCTTAATATGTGATATTTTGTAT  
36341 ATGGATACCAATAGTAAATTAATAAATCACTAGTAGACTTATAAATAGTAGCACTATAGATGATGATGAAAACCTTGAAACAGCAT  
36433 GTTGTGTCGGGTGAAGACCAAGAGAGACATGATTTTGGAAAGTCTTGCTGTGATTTCTTGAGAAATCACTGTAGAGATGGCGTTAA  
36525 ATAAAGTACTCTCCACAGAGGTGAATCCAGCCATATCTACTGTATGATGTCTTTTATGATCCTCAATGATGTTAGGATGAGCTTAT  
36617 TAGTGAGCATGTAAGGATGGCTCTTGAGGTACAGGTTCTTTCAGTGAGATGCAATCTCATAGCTTTATCTCATGTTCTCAAGTGGGCC  
36709 AGAAGGTGCTGAGAATGCCAAGCAGCATGCCAAGACTAGGACAGTATAGAATGCCATTGCTTGGGCAAGCAGGTAAAGAACACCTTTT

36801 ATACCTTTTAAATGCATATAGATAGGTGCATGGATGGGTCAATAGGCCATTCTGTTTGTGTGTCTAGAGACAAAGAGGATTTGAATGTGTA  
36893 AACTGAGAAATACATAAGCCAGATTTTGA AAAATCAITTTGGTAGAGTCACAGAGGATAGCACTGTCTGGAGAAATGCTCACTTGGAAAC  
36985 TGGCAGGGTGCCAGCTAGTGTGATCTGCAGAGCTGGGATTC AAGGACCAACACATGCTCCAGCTGAGAGTCAGGGCAATCTCAGTGAAGGC  
37077 CTGGGGTGATCTTTATCTCTGTACTTACTTGTGAAGCATTTGACTTGTGTATATTGTTTCTTAAGCACAAGCCATTGGCTGGAATGTTTT  
37169 CTATGTAAATTTGATTTAGTTGTCTCATCCCATAGATGTTTTCCATGTTTTTATAGATATGAGATTTCTGTGGCTTAGGCCAATGGAATAA  
37261 TAATTAGACTTCTCATAGAAATGAGACTATAAATGAATTGATTTGGTGTCTTGGAAACCAGTTGAGCAATTTCTCAAAACCTTGAGAAGAA  
37353 GACATTTGTTTAAGGATGCATCTGGAATCTTGACAAAATGCCAGATTTTCTGCCATCTACAGGCAGACAGCAATAAGCTATCCAATGATG  
37445 ACATGCTCAAGTTACTTGCAGATTTCTGGAGATGAGTTTCAAGGCTTATTTGCCACAGCTGAAAAATGAGAGCTGTGTAGTGGGAGGGAGG  
37537 AAGCAGGGGACAGCTCACTAGGTTGCTCTGATTAGACATCAGAGGGGATGCCAAATGAGCTGTGAGCAATTTCTCAAAACCTTGAGAAGAA  
37629 GATGGGTGAAAATCAGAGAATAACCAGTTAATTTGAATTTCTGTAGAGGATGTTTTGGTGGTGTCTGTGAAGGTTGGCATGGTGAAGATG  
37721 AGCCTATGGTGGGGAGAAACAGTTGAGGAACCTTGTCAAGAGGTGAGAAGGACTACGCAAAAGCCACTCGAAGTGCAAAACGGAAGAGGG  
37813 GACAAATTCAGTGTGCTGCAAGAGATACGATGACTGGGCTTGGCTTGGGTGGTAAATGCTAAGATAAATAACTTGCAGGTTTCTAAC  
37905 TTGGAAATTTCTGGCCACAGTTGTTGCTTAGCTTGTGGCAGCATGCTCCACTTGCCTTGGCTCCACATGGTCTCTCTCTGTGTCTC  
37997 TGTCTAAATTCCTTCTAGAACATAGTATAAAGCATCAGGCCCAAGCTAGTGACCTCATCTTAACCTGATTGCATCTGCAGAGACCCCTG  
38089 TTTCCAAATAGGTACATTTATAGGTACAAAAGGGTTGGGACTTCACCATGCTTTTGGAGGACAACTCAACCCATAACATAAGGCAATAA  
38181 GGGAGCAAGGAATGTGTCAACATCAGAGGGCGGGCAGCTTCCCAAGTCAGTCTCACCCAGGGGCTGTGTCTTAACTCTATGCTGTGTT  
38273 TGCCTGCTACCTCTAAGAGTCTCACTCTGAACCTTTTGAACCTGATTTTCTTCTAGGAGATGGGTCTAGAATTTTCTGGGAAATTTCT  
38365 GGAATGTGAAGAGCTGAGGGCGCTAGAAGATGTGAAGTGAAGAATAGCTGAGAGCCAAATGCTAACTATTCTATGCGGAAGGTATCTCT  
38457 TGTTTTTTTTTTTTTTTGTGCATATCAAAATAGCAATCTTATCAGTTTGTCTAGAACTCAAGAATGATGCTTACCTTTCTTAACTCTTAT  
38549 TTACCTTTTCTTATCTGTCTTCTAGTAGTAGGAATAGAAACGATATGATGATGACAAACAGGCTCAATAAGTTCTGGAACACAGAGACGTG  
38641 TTCTAATCAGAAATCAATCAAGTCCATGTGACAGGGCGGCTTCAGCCTTCACAGCAGAGTGAAATCCCTTGTCAAGAGGCTCAAAAAGGTA  
38733 GAAAGGATTTCTCAAGGCTCTTTTCAGTTATGTGATTATACAGTTTGTGACTGTCTGATGTTTCCCTGTTTGGAGCTTTAATGAGAATGTC  
38825 AACTCAGTTTGTCTAATCAGTCAGTAAATGATGTTGCCCTGTTCAGCAAGACAGTGTGATGCGCCGCTGGGCTGATTTGGAATGAACCTTTCACA  
38917 GCTCAGCTAGGGAATGTGAGAGAGGGGAGAGGAGGATACTGGTGAAGGATGAGGCTGCTGGGTGAGCCTTCAGGGTCTCTGACCATAATA  
39009 GGTGCCCCAAATCCCATCTCTGCAGTTTATGACCTGGTAAGGACACAGGCTTGGCCAGGAGGTGCCCTGGATCCCTATGAAAT  
39101 CTGTATTTCTTAAGAGCTAAATAAAGATATAGTACCCATTTTACTTTTAAATCAGATAGTTCTTGTAGTTACAAACATAATACATGTT  
39193 CATTTTGAAGAATTTGAGAAATACAGAGAATAAAGGATGAAAAGGTTTACTACTAGTTTATTAACCTCTGCTGGTGAACCTTTTGGAGACT  
39285 TTTTTTTTTTTTTTGTAGATGGAGTCTCACTCTGTCCCTCAGGCTGGCGTACAGTAGGCAGATTCAGCTCACTGCAACCTCCGCCCTCCCGAG  
39377 TTCAAGCGATTCTCTGCTCAGCCTCCCAAGTAGCTGGGACTATAGGCGCCACCCTACGCTGGCTAAATTTTGTATTTTATGTAGAGA  
39469 TGGGGTTTCAACATATTGGCCAGGCTGATCTCAAACTGCTGACCTTGTGATCTGCCGCCCTCAGCCTCCCAAAGTGCTGGGATACAGGCAT  
39561 GCGCACCGCTGCGCAGCTAGGGGAGCAATTTTTTTACGTTTATCTCTTATGTTTATTTAGTTTCTTATGAGTATGATGATTTAT  
39653 ACTAATATGTAATATTTCCTGCAACACTCAAGTATTTTCTGAAAGTGTTATATATACATTTTATAGACATCATTTTATGCAATAAATA  
39745 TTATAAATGTCCATTCAGATAGACCATGATATTTTAACTCTTCCCAATTTTGTACTTTTTTTTTTTTTTCCGAGATGGAGTCTGCTCT  
39837 GTCGCCAGCTGGAGTGAGTGGCCACCTCTCAGCTCAGTCAACCTCCGCTGCCAGGTCAAGCAATTCCTGCTGCCAGCTCCGTAGT  
39929 AGCTGGGACTCCTGAGTAGTGTAGTACGCCATGCTGCCAGGCCGCCCTAAATTTTTTTTTTTTTTTTTTTTTTTTGTATTTTATGTAGAGA  
40021 TACTAAATATCTCACCATCTTGCCAGGCTGGTCTCAAACTCCTGACCTCAGCAATCTGCCCGCTCAGCTTCCCAAAGTGCTGGGATTA  
40113 AGCTGTGAGCCACCATGCCGACCAITTTTGTACTTTTAAATGTGTTCTGATTTTACAGATATACCTTAGGCAACAGTTAGAACTTTTGA  
40205 AAAAATCTTCTCTATTGGTAGTGGGTAAATATATATCATACATATATATATACATATAGTAATTAATGTCAATTTTGTAGTTTTCAGAAA  
40297 ATTTCACTTTCTACTAATTTTCAA AAACAGTCACCTTTAGTTGGATAGATTTCAATATTTTCTTCCGCTCAACTACCATGCAACTCTTAA  
40389 TAACTCAGAGGTGGGTCTGGGTGATCTAGGAAGGTGAATACACTATATTAATAGGAAGAAAATATATCTGTATGATCTTATTTTGA  
40481 AAGAAAATATATATTCTTTTGTATGAAATGAAGAAATGGATAAGCAAGTAGCTATCTAGATGGAAGATAGGCATAAAAATAGCTATTTA  
40573 GGATATATGCCAAATAGATGTTATCTCTGAGGCTGGGTGATGGGTGATATTTCACCTTCCACTTTATTAACATCTGTCAATTTTATTA  
40665 TGAACCTTTAAAAAATCAACCTTTTATATTACAGACAAAACAAATGAAGTTTTCATTTGATGGAGTTGGAGCCCTGTCTCAAGAG  
40757 TTAICTCTTAGGCTGGTAGCTTGTAGACTTCCCAACAGTGGCGGCTCTCAGAGGCGACGCCAGTGTGATGTCCTGTCTTCAAGTGGAGGCT  
40849 GGGAGTGGGCTTCACATGTGCACTAATTTGAAGTAGTGGGAGCAAGAGGCTGTGGCCAGGCAAGAGGCGCCAGGAAAACAGAGTGT  
40941 GAGTCTCTCTGACACACCACTTCTTATGATGATGCTCAGCAGGAGGGCATTTGGTGTGAAGGTTGTGCTCCAGGTGGCCAGTTAGAGACCC  
41033 AGAAACTGTGAAGACGGGATGCGATGTGACAGCTCAGCAGATAGAAGACACAGCAGGATAGTGAAGGCCACCTCTCTCAATGAATATCAAAAAGAACT  
41125 TTGGTGGCCACTCCCGATTTCTTCAACAGAGTATAGGGGAGCTGGAGGATTCCTTTTCAATTTTAAAAAATCTTGCATGCTGATTTT  
41217 CTTCCTCTGTATATTTTACAGGAAATAATCTCATGTGAGTGGCTGGCCACGGCTTGGATCCAAGCTATTGTTTCTACCCCATGATTG  
41309 TCTCAAAATGTTATTTAATGATGATGAAAAAATTTCTCACGCTGTCTCAGTCTTAAACAAACAGCTGCCAAAGCTCATAGGCCATTTCT

FIG. 12B

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41401 CTTTTCCCTTGCAATAATTACCCAGGGATATGTTCCAAGATTAGTAAGAAAGCGATTCTGTCGATAGATGATATTGCTAACATTTTATA  
 41493 AGAAGAGAGACTTGGTACTTTGTATTGATTTGTTTCATGGTGGTATCTCATGGATAAGATGGTATCTCATCTTTTCCAACCTTCTCGAGGAAA  
 41585 TGGGAGACATGAAGGCAAGTATAAAATAGAACGTTTCTTTAAAACGTAGACCTTTTAAATGGTACTACGTTGGATAGTTTAGGTAATA  
 41677 ATACTACTAAAGTTTTTGGTATGCAGCTTAATGTGCTGTGTTTATTGTACACTCATCTTCTTGCACTCCAGGTTTTACAGCTCTTACCCC  
 41769 GATTTCGCTCTGGTTACACTGCATCAAGCCAAGTAGGGCTGCTTGACTTCTCTAAACCCACTGGGGACTTCCCTCTGCGCATGCTTTTCTC  
 41861 TCTGCCAAATTGTGCCCCCTTCCTGCCCTCATCAAGCAGCACATAAATCACAAAACATGCAGCATACACACTTCCCTTTTCTTTGTCTT  
 41953 TCTCAGGGAACCTCTACTCATCTTTCAAAGCCAGTCTGTGGCTCACTTCTGTGCTGGAGTCTCGAGGCGGTTACTTGGCTTCTCTGCCCTG  
 42045 AGCCGCTCCTCTTTTAAAGGCGGATAATAACAGCCCTGCCCCATAAAACCGTGGTGGGAATAAATGCAAAAGGCATTAAAGTGATTTC  
 42137 TCCCACCATGAATACTGATCTCATCCCGTGTCCCTCTCGATAGATCTAGATACTCTGCCCTTCTGGTAGAGTTTGTACATACTCTGTGAAA  
 42229 GTGATTGCCCTCATATGCGCTAAGTAGCTTACAGTGTCTACTGGACTTTTGGCTTCTTGAGGAAAGAAATATGTCTTGTTCGATTCTCTCC  
 42321 ATGGTCTGAGTACATACATTGACGATATCCTAAGCACTTGATAAATGCTTATTGAATTTTCTTCTAGACATAAACTCAGTGGTTTTGT  
 42413 TGAACAAAAATATCTCAAATTTCTTTCAATCATATATAGTTGTTTTTTTTTAAAGTGACACAAAGCTTTTAGGGAATATTTCTTTTCCAA  
 42505 AACACAGTTAGAAGATTAACCTACCACCAATAGCAGTCCAAACATACCTGTATTGCCAGCTAATCATTTTAACGAGCCAATACAGGAAGTC  
 42597 AGGAAGGGAAGACCGGCTGCAGAAACACTTAGATAAGGACCCCAATCTGTTGGCATGGGAGGACTGCTAGTTGATGATACCATTCCCATTT  
 42689 CCTCTGTGGGAATTGTTAGTCAGCAGAAATGGTGGCAGTGGGAAGGAAAAATTTCTTAAGAGAGAGTTTGAGCCTCACTTCTACATTC  
 42781 ACACAGAGACAGGAGCAGTCCAGAGGCCAGGCATCTGCAAGTGTCTGTATTGCATGCTTACTTAAATCGTGTAAATTTAAGATGAGTTT  
 42873 TCAATGTTCAAGGATTATTTTATAAATTTTGCATAGAATATAGGTACTCTTTAGCAAAACAAAGCAAAAAAACCAAACTATTCTCAGTCATG  
 42965 AAAGAATTCAAGTTTGTGTACACGCACACACACCACACTTTGGAAGTGCAATAAAAGGCAATAAATCTTTATTGCTGTGAGTGTGTTGATG  
 43057 TCTAATAAACAGATTCAACATAAACCATAACTTTTGAATGGGTTTGAGATTGGGTTTTTAAAAACTTAAAGCTGGCAAAAAAAAACA  
 43149 ACTTTTAAAGCCCATGTGCTACATAATATGGAACTAAACTCAGAAATGTGCTTGGAAACACATGGAAGAACGCTCTTACAGAACGACGAA  
 43241 CTAGAAGTAAATCTCTCAGCAGAGGGAGGAAATAGAATAAGAAATAACTATAGTTAGGCACAGAGGACACATAACATATAGGAAGATTT  
 43333 CCAAGTGAAGATCAITTAATTAATAATGTTGCTTAGAAACGTATTTAAATTGTGTTCCACCTCTCTCAAAAATTTATATGTGGAGGATGTG  
 43425 GAGTGATCTTAAAAATGGTGATGAAGTGCTGTCAITTCATAGGTGGAATAAATTAGGAGGGGTGAAATCCATTACCTTGCATACCTAC  
 43517 TTATATTTAAAGTATAATTTGTAATAAA





hCLASP4	FKSHLESTIYTQDLHVHKFFHHCOLIQS-----	-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLES	SVTFPIRVLDQKISMALEHEKLKLSIICLNSS	715
hCLASP3	VEVVAVSSIHQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS		780
hCLASP2	ISTHLVSTVYTDQDLHNFQYQCKTES-----	-----GAQALGNELVKYLSKLHAM	787
hCLASP7	VELTAVSSVHPDPYLDKFFTLVHVEES-AFPFRLKDTVLSEGNVEQELRASIAALRLA		767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREKD-----	-----MSQSPTSNIIRSCNLLNVE	887

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hCLASP4	EIDVMIQFLPVIILMQLER-----	-----VLTNMTM-----	EDDVP	824
hCLASP5	RLEPVLVFLHLVLDKLFQLSVQPMVIAGQTANFSQAFESVVAIANSLHNSKDLKSDQHG			775
hCLASP3	QLEPVVRFLLHLLDKLILLVIRPPYIAGQIVNLGQASFEAMASINRLHKNLEGNHDOHG			840
hCLASP2	EGHVMI AFLPTILNQLER-----	-----VLT-RAT-----	QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEMAHVSVLVHRSLEAAQDARG			827
hCLASP1	KIHAIMSFLPIILNQLER-----	-----VLVQNE-----	EDEIT	916

.. : : \* : : \* : : \*

hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----	-----YLRSFIKYS-----	FRPEKP	860
hCLASP5	RNCLLASVYHVFRLEPVQDVPKSGAPTALLDPRS YHTYGRTSAAAVSSKLLQARVMSS			835
hCLASP3	RNSLLSYIHVFRPLNTYPNSSPG-PGGLGGSVHYATMARSASVRPASINLNRSLNS			899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----	-----HLRSYVYKA-----	YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP-----	-----VTVQAATLARGSGRPASLYLARSKISS		883
hCLASP1	TTVTRV-LPDIIVAKCHEEQLDH-----	-----SVQSYIKFV-----	FKTRAC	952

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hCLASP4	SAPQAQLIH-----	-----ETLATTMIAILKQS-----		883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNCSRMSSYYCSGSSDAPSSPA-----			882
hCLASP3	SNPDISGTPSPDDEVSRIIGSKGLDRSNSWVNTGGPKAAPGWSNPSPSAESTQAMDRSC			959
hCLASP2	VASEYKTVH-----	-----EELTKSMTTILKPS-----		875
hCLASP7	SNPDLAVAPGSDDEVSRI LASKLLHEELA-LQ-----			915
hCLASP1	KE---RPVH-----	-----EDLAKNVTGLLKS-----		972

:

hCLASP4	-----	-----ADFLSINKLLKYS-----	-----WFFFEIIAKSM	907
hCLASP5	-----	-----APRPASKKHFEELALQ-----	-----MVVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLTGLPTKKLFHEELALQVWCSCSVRESALQQAFFFEILMVKSM			1019
hCLASP2	-----	-----ADFLTSTNKLRLYS-----	-----WFFFDVLIKSM	899
hCLASP7	-----	-----WVVSASVREAILQHA-----	-----WFFFQLMVKSM	942
hCLASP1	-----	-----DSPITKVHLKHS-----	-----WFFFAILLKSM	995

# Cadherin Cleavage

hCLASP4	ATYLLLENKIKLHGGORFPETVHHVHLSLLAIIPHVTIRYAEIPDE---SRNVNYSLAS			964
hCLASP5	AQHVNMDKRDSDRRTRFSDREMDDITTVNVVTSEIAALLVKPKENEQAEKMNISLAF			970
hCLASP3	VHHLYFNDKLEARRKSRFEREMDDIAALVSTIASDIVSRFQKDTM---VERLNTSLAF			1076
hCLASP2	AQHLIENSKVLIRNQRFPSYHHAETVVMMLMPHITQKFGDNPEA---SKNANHSLAV			956
hCLASP7	ALHLLLGQRLDTERKLRFPGRLDDITALVGSVGLVITRVHKVDVL---AEHLNLSLAF			999
hCLASP1	AQHLIDNTKLRPQRFPESYQNELDNLMVLSDHVIWIKYKDALEE---TRATHSVAR			1052

.. : : \* \* : : : : : : \*

hCLASP4	FLKRCFLTMDRGFIENLINDYISGFSKDP-----	-----MVLAEYKFEFLQTCNHEHYIPLNL		1019
hCLASP5	FLYDLLSLMDRGFVNLI RHYSQLSAKLSNL-----	-----FTLISMRLFEFLRLCSHEHYIPLNL		1027
hCLASP3	FLNDLLSVMDRGFVPSLIKSCYQVSSKLYSLPNPSVLVSLRLDFLRIICSHEHYITLNL			1136
hCLASP2	FIKRCFTFMDRGFVFKQINNYISCFAPGDP-----	-----KTLFEYKFEFLRVVNCNHEHYIPLNL		1011
hCLASP7	FLSDLLTMDRGFVSLVRAHYKQVATRLQSSPNPALTLRMEFTRLCSHEHYITLNL			1059
hCLASP1	FLKRCFTFMDRGCVFKNVNNYISMFSGDL-----	-----KTLQCYKFDLQEVQCHHEFIPLC		1107

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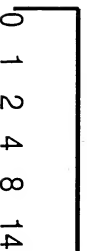




# Human CLASP-2 expression in T cells upon activation

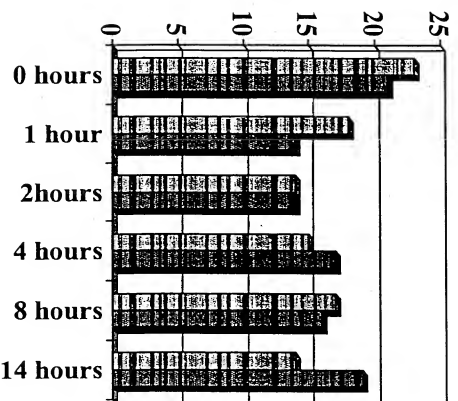
**A)**

hours post  
activation



**B)**

% of total  
signal



CLASP-2 (A)  
CLASP-2 (B)

~7.5 kb -

CLASP-2

2.5 kb -



28S rRNA Ethbr. staining

TT TTT ACC AAG AAG AAA GAT TTG TTC AGC CTG GTG ACG CTT CAG AAG AGA AGA GTT -52  
1  
TAA CGA CAT TGA TAT TTT GAA ATA TTT TGT GAC TCA AAT TAT AGC AAT ACG ATG AGT TTT 9  
met ser phe

CGA GGG AAG GTT TTT AAA CGG GAG CCC AGT GAA TTT TGG AAG AAG AGA CGA ACT GTG AGG 69  
arg gly lys val phe lys arg glu pro ser glu phe trp lys lys arg arg thr val arg

AGA GTA ATC CAA GAA GAA TTC CAC AGA TTT AGT TCT CAA GAA AAG CCT AGG CTT CTC GAG 129  
arg val ile gln glu glu phe his arg phe ser ser gln glu lys pro arg leu leu glu

CCT TTG GAT TAT GAG ACT GTC ATT GAA GAA CTT GAA AAG ACC TAC CGG AAT GAT CCT CTT 189  
pro leu asp tyr glu thr val ile glu glu leu glu lys thr tyr arg asn asp pro leu

CAA GAT CTC TTG TTC TTC CCC AGT GAT GAC TTT TCA GCA GCC ACA GTT TCC TGG GAT ATC 249  
gln asp leu leu phe phe pro ser asp asp phe ser ala ala thr val ser trp asp ile

CGC ACG TTG TAC TCA ACA GTA CCT GAA GAT GCA GAG CAC AAG GCA GAA AAT TTA CTG GTT 309  
arg thr leu tyr ser thr val pro glu asp ala glu his lys ala glu asn leu leu val

AAG GAG GCT TGT AAA TTT TAT AGT TCC CAG TGG CAT GTG GTA AAC TAC AAA TAT GAA CAA 369  
lys gly ala cys lys phe tyr ser ser gln trp his val val ser trp lys tyr glu gln

TAT TCT GGA GAC ATT CGA CAG CTA CCC CGA GCA GAA TAC AAA CCA GAG AAG CTT CCT TCA 429  
tyr ser gly asp ile arg gln leu pro arg ala glu tyr lys pro glu lys leu pro ser

CAT TCC TTT GAG ATT GAC CAT GAA GAT GCT GAT AAG GAT GAA GAT ACC ACT TCC CAC TCG 489  
his ser phe glu ile asp his glu asp ala asp lys asp glu thr thr ser his ser

TCT TCC AAG GGG GGT GGA GGA GCG GGA ACT GGT GTT TTC AAG TCC GGC TGG CTC TAC 549  
ser ser lys gly gly gly gly ala gly gly thr gly val phe lys ser gly trp leu tyr

AAG GGG AAT TTT AAC AGC ACC GTG AAC AAC ACC GTT ACT GTT CGG TCA TTC AAA AAG CGC 609  
lys gly asn phe asn ser thr val asn asn thr val thr val arg ser phe lys lys arg

TAC TTC CAG CTG ACT CAG TTA CCA GAT AAC TCC TAC ATT ATG AAC TTT TAC AAA GAT GAG 669  
tyr phe gln leu thr gln leu pro asp asn ser tyr ile met asn phe tyr lys asp glu

AAA ATA TCC AAA GAG CCC AAA GGA TGC ATC TTT TTG GAT TCC TGT ACA GGA GTG GTG CAG 729  
lys ile ala ser lys glu pro lys gly cys ile phe leu asp ser cys thr gly val val gln

AAT AAC AGA CTA AGA AAA TAT GCC TTT GAA TTG AAA ATG AAT GAT CTG ACC TAT TTT GTG 789  
asn asn arg leu arg lys tyr ala phe glu leu lys met asn asp leu thr tyr phe val

CTG GCA GCT GAA ACA GAG TCA GAT ATG GAT GAA TGG ATC CAC ACC CTC AAC CGC ATT CTG 849  
leu ala ala glu thr glu ser asp met asp glu trp ile his thr leu asn arg ile leu

CAA ATC AGT CCT GAG GGG CCC CTC CAA GGG AGG AGG AGC ACA GAG CTC ACT GAT CTG GGT 909  
gln ile ser pro glu gly pro leu gln gly arg arg ser thr glu leu thr asp leu gly

CTG GAT TCG CTG GAT AAT TCT GTA ACT TGT GAA TGC ACG CCA GAG GAA ACA GAT TCT TCA 969  
leu asp ser leu asp asn ser val thr cys glu cys thr pro glu glu thr asp ser ser

GAG AAC AAC CTA CAC GCA GAC TTT GCA AAG TAC CTC ACA GAA ACA GAA GAT ACT GTA AAA 1029  
glu asn asn leu his ala asp phe ala lys tyr leu thr glu thr glu asp thr val lys

ACA ACT CGA AAC ATG GAG AGG CTA AAT CTG TTC TCT CTA GAT CCA GAC ATA GAT ACC TTG 1089  
thr thr arg asn met glu arg leu asn leu phe ser leu asp pro asp ile asp thr leu

AAA CTT CAA AAA AAA GAT CTC TTG GAA CCT GAG TCT GTG ATC AAA CCA TTT GAA GAA AAA 1149  
lys leu gln lys lys asp leu leu glu pro glu ser val ile lys pro phe glu glu lys

FIG 15/1

GCT GCC AAG AGA ATC ATG ATC ATC TGT AAA GCC CTC AAC TCA AAT CTT CAG GGA TGT GTT 1209  
 ala ala lys arg ile met ile ile cys lys ala leu asn ser asn leu gln gly cys val  
 ACG GAG AAT GAA AAT GAT CCG ATA ACG AAT ATT GAG CCT TTT TTT GTG AGT GTG GCA CTT 1269  
 thr glu asn glu asn asp pro ile thr asn ile glu pro phe phe val ser val ala leu  
 TAT GAC CTC AGA GAC AGC AGG AAG ATT TCT GCT GAT TTT CAT GTG GAT CTA AAC CAT GCT 1329  
 tyr asp leu arg asp ser arg lys ile ser ala asp phe his val asp leu asn his ala  
 GCT GTC AGA CAG ATG CTC TTG GGG GCT TCT GTG GCT TTG GAA AAT GGC AAC ATC GAC ACC 1389  
 ala val arg gln met leu gly ala ser val ala leu glu asn gly asn ile asp thr  
 ATC ACT CCA AGA CAA TCA GAA GAA CCT CAC ATC AAG GGA CTT CCA GAG GAA TGG CTA AAA 1449  
 ile thr pro arg gln ser glu glu pro his ile lys gly leu pro glu glu trp leu lys  
 TTT CCA AAG CAG GCT GTA TTT TCT GTA AGC AAT CCA CAT TCT GAA ATT GTT TTG GTG GCC 1509  
 phe pro lys gln ala val phe ser val ser asn pro his ser glu ile val leu val ala  
 AAA ATC GAA AAA GTC TTG ATG GGA AAC ATT GCA AGT GGT GCC GAA CCT TAT ATT AAG AAC 1569  
 lys ile glu lys val leu met gly asn ile ala ser gly ala glu pro tyr ile lys asn  
 CCA GAC TCC AAC AAG TAT GCA CAA AAG ATA CTA AAA TCC AAC AGA CAA TTC TGC AGC AAA 1629  
 pro asp ser asn lys tyr ala gln lys ile leu lys ser asn arg gln phe cys ser lys  
 TTG GGA AAA TAC CGA AGG GCT TTT GCT TGG GCA GTA AGA TCA GTA TTT AAG GAC AAC CAG 1689  
 leu gly lys tyr arg arg ala phe ala trp ala val arg ser val phe lys asp asn gln  
 GGA AAT GTG GAC AGA GAC TCA AGA TTT TCA CCA TTG TTT AGA CAA GAA AGT AGC AAG ATT 1749  
 gly asn val asp arg gln phe ser pro leu phe arg glu phe cys ser lys ile  
 TCA ACT GAG GAC CTA GTT AAA CTA GTA TCA GAT TAT AGA AGG GCC GAC AGA ATA AGC AAA 1809  
 ser thr glu asp leu val lys leu val ser asp tyr arg arg ala asp arg ile ser lys  
 ATG CAG ACC ATT CCT GGA AGC CTG GAT ATT GCT GTT GAC AAC GTT CCT TTG GAG CAT CCA 1869  
 met gln thr ile pro gly ser leu asp ile ala val asp asn val pro leu glu his pro  
 AAT TGT GTA ACA TOG TCC TTT ATC CCT GTC AAG CCT TTC AAC ATG ATG GCT CAA ACA GAA 1929  
 asn cys val thr ser ser phe ile pro val lys pro phe asn met met ala gln thr glu  
 CCC ACA GTG GAG GTG GAA GAA TTT GTT TAC GAT TCA ACA AAG TAT TGT CGG CCT TAC AGA 1989  
 pro thr val glu val glu glu phe val tyr asp ser thr lys tyr cys glu pro tyr arg  
 GTA TAT AAA AAT CAA ATT TAT ATT TAC CCC AAA CAC CTC AAG TAT GAT AGC CAG AAA TGC 2049  
 val tyr lys asn gln ile tyr ile tyr pro lys his leu lys tyr asp ser gln lys cys  
 TTC AAC AAG GCA CGG AAT ATA ACT GTG TGC ATT GAA TTC AAA AAT TCA GAT GAA GAA AGT 2109  
 phe asn lys ala arg asn ile thr val cys ile glu phe lys asn ser asp glu thr ser  
 GCC AAG CCC CTG AAG TGT ATT TAT GGA AAA CCT GAA GGG CCC CTC TTC ACC TCA GCC GCC 2169  
 ala lys pro leu lys cys ile tyr gly lys pro glu gly pro leu phe thr ser ala ala  
 TAC ACA GCA GTT CTG CAC CAC TCT CAG AAT CCG GAT TTC TCA GAT GAG GTG AAA ATT GAG 2229  
 tyr thr leu his his ser gln asn pro asp phe ser asp glu val lys ile glu  
 CTA CCA ACA CAA CTC CAT GAG AAA CAC CAT ATT TTG TTT TCT TTT TAT CAC GTC ACC TGT 2289  
 leu pro thr gln leu his glu lys his his ile leu phe ser phe tyr his val thr cys  
 GAC ATC AAT GCA AAA GCT AAT GCC AAA AAG AAG GAG GCT CTG GAA ACG TCA GTT GGA TAT 2349  
 asp ile asn ala lys ala asn ala lys lys lys glu ala leu thr ser val gly tyr  
 GCT TGG CTT CCT CTG ATG AAA CAC GAT CAG ATA GCT TCT CAA GAG TAC AAC ATC CCA ATA 2409  
 ala trp leu pro leu met lys his asp gln ile ala ser gln glu tyr asn ile pro ile

FIG 15/2

GCA ACA AGT CTG CCT CCT AAT TAT TTA AGC TTT CAA GAT TCT GCA AGT GGA AAG CAT GGT 2469  
 ala thr ser leu pro pro asn tyr leu ser phe gln asp ser ala ser gly lys his gly  
 GGG AGT GAC ATT AAA TGG GTT GAT GGT GGC AAA CCA CTT TTC AAA GTG TCG ACA TTT GTT 2529  
 gly ser asp ile lys trp val asp gly gly lys pro leu phe lys val ser thr phe val  
 GTA TCA ACA GTA AAT ACT CAG GAT CCA CAT GTG AAT GCA TTT TTC CAA GAG TGC CAA AAA 2589  
 val ser thr val asn thr gln asp pro his val asn ala phe phe gln glu cys gln lys  
 AGA GAG AAA GAT ATG TCT CAG TCA CCT ACC TCA AAT TTC ATC CGC TCT TGT AAG AAC TTA 2649  
 arg glu lys asp met ser gln ser pro thr ser asn phe ile ser cys lys asn leu  
 TTG AAT GTG GAA AAG ATT CAT GCA ATC ATG AGT TTT CTG CCT ATA ATT TTG AAT CAG CTC 2709  
 leu asn val glu lys ile his ala ile met ser phe leu pro ile ile leu asn gln leu  
 TTC AAA GTT CTG GTA CAG AAT GAG GAA GAT GAA ATA ACT ACA ACT GTC ACC AGG GTT CTG 2769  
 phe lys val leu val gln asn glu glu asp glu ile thr thr thr val thr asp val leu  
 CCC GAC ATT GTG GCC AAG TGC CAT GAG GAG CAG CTG GAT CAT TCT GTC CAG TCA TAT ATT 2829  
 pro asp ile val ala lys cys his glu glu gln leu asp his ser val gln ser tyr ile  
 AAG TTC GTG TTC AAG ACC AGG GCA TGC AAG GAG AGG CCT GTA CAT GAG GAC CTG GCT AAA 2889  
 lys phe val phe lys thr arg ala cys lys lys glu arg pro val his glu asp leu ala lys  
 AAT GTG ACT GGT CTT TTG AAA TCA AAT GAC TCA CCA ACA GTA AAG CAT GTC CTA AAG CAT 2949  
 asn val thr gly leu leu lys ser asn asp ser pro thr val lys his val leu lys his  
 TCC TGG TTC TTT GCA ATT ATC CTA AAA TCG ATG GCA CAG CAC TTG ATT GAC ACA AAT 3009  
 ser trp phe phe met phe ala ile leu lys ser met ala gln his leu thr pro ser thr asn  
 AAA ATC CAG CTT CCC CGG CCT CAG AGA TTT CCT GAA TCT TAC CAA AAT GAA TTG GAC AAT 3069  
 lys ile gln leu pro arg pro gln arg phe pro glu ser tyr gln asn glu leu asp asn  
 CTT GTC ATG GTC CTA TCC GAC CAT GTG ATT TGG AAA TAC AAG GAT GCC CTT GAA GAA ACA 3129  
 leu val met val leu ser asp his val ile trp lys tyr lys asp ala leu glu glu thr  
 AGA AGG GCA ACC CAC AGC GTT GCC AGA TTT CTC AAG CGC TGC TTT ACA TTT ATG GAC CGG 3189  
 arg arg ala thr his ser val ala arg phe leu lys arg cys phe thr phe met asp arg  
 GGG TGT GTG TTT AAG ATG GTC AAC AAT TAC ATC AGC ATG TTC TCC TCC GGT GAC CTT AAG 3249  
 gly cys val phe lys met val asn asn tyr ile ser met phe ser ser gly asp leu lys  
 ACC TTG TGC CAG TAT AAA TTT GAT TTT CTT CAA GAA GTA TGT CAA CAT GAA CAC TTT ATC 3309  
 thr leu cys gln tyr lys phe asp phe leu gln glu val cys gln his glu his phe ile  
 CCT TTG TGT CTG CCC ATA AGA TCA GCA AAC ATT CCA GAT CCT TTG ACA CCT TCA GAA TCG 3369  
 pro leu cys leu pro ile arg ser ala asn ile pro asp pro leu thr pro ser glu ser  
 ACT CAA GAG TTA CAT GCA TCA GAT ATG CCT GAA TAT TCA GTC ACA AAT GAA TTT TGT CGG 3429  
 thr gln glu leu his ala ser asp met pro glu tyr ser val thr asn glu phe cys arg  
 AAG CAT TTC TTA ATC GGA ATT CTG CTC CGA GAA GTT GGC TTT GCC CTG CAG GAA GAC CAA 3489  
 lys his phe leu ile gly ile leu leu arg glu val gly phe ala leu gln glu asp gln  
 GAT GTC AGA CAC TTA GCT TTA GCT GTC CTA AAA AAT CTA ATG GCT AAG CAT TCA TTT GAT 3549  
 asp val arg his leu ala leu ala val leu lys asn leu met ala lys his ser phe asp  
 GAT CGA TAC AGA GAG CCA AGA AAG CAG GCC CAG ATA GCA AGT TTA TAC ATG CCC CTG TAC 3609  
 asp arg tyr arg glu pro arg lys gln ala gln ile ala ser leu tyr met pro leu tyr  
 GGC ATG CTC CTG GAC AAT ATG CCA AGG ATT TAT CTG AAG GAC CTG TAT CCT TTT ACT GTC 3669  
 gly met leu leu asp asn met pro arg ile tyr leu lys asp leu tyr pro phe thr val

FIG 15/3

AAT ACA TCT AAT CAG GGG TCT AGA GAT GAT CTA AGC ACC AAT GGA GGA TTT CAA AGC CAG 3729  
asn thr ser asn gln gly ser arg asp asp leu ser thr asn gly gly phe gln ser gln  
ACA GCT ATC AAA CAT GCA AAC TCT GTG GAT ACA TCA TTT TCT AAA GAT GTT TTA AAT TCC 3789  
thr ala ile lys his ala asn ser val asp thr ser phe ser lys asp val leu asn ser  
ATA GCA GCA TTT TCA TCA ATA GCT ATT TCT ACA GTA AAC CAT GCT GAC TCC AGA GCA TCT 3849  
ile ala ala phe ser ser ile ala ile ser thr val asn his ala asp ser arg ala ser  
TTA GCA AGT CTT GAC TCC AAT CCA AGT ACC AAT GAG AAG AGC AGT GAG AAG ACG GAC AAC 3909  
leu ala ser leu asp ser thr asn glu lys ser thr ser glu lys thr ile ser  
TGT GAA AAG ATC CCA AGA CCC TTG GCT TTG ATT GGC TCA ACT CTT CGA TTT GAC AGG TTA 3969  
cys glu lys ile pro arg pro leu ala leu ile gly ser thr leu arg phe asp arg leu  
GAT CAA GCA GAA ACC AGG AGT CTC CTG ATG TGT TTT CTT CAC ATT ATG AAA ACG ATT TCG 4029  
asp gln ala glu thr arg ser leu leu met cys phe leu his ile met lys thr ile ser  
TAC GAG ACT CTG ATT GCC TAC TGG CAG AGA GCT CCC AGC CCA GAG GTG TCC GAC TTC TTC 4089  
tyr glu thr leu ile ala tyr trp gln arg ala pro ser pro glu val ser asp phe phe  
AGC ATC TTG GAC GTT TGT CTT CAA AAT TTC AGA TAC CTA GGA AAA CGC AAC ATA ATA AGA 4149  
ser ile leu asp val cys leu gln met asn phe arg tyr leu gly gln asn ile ile arg  
AAA ATT GCT GCT GCA TTT AAA TTT GTG CAG TCC ACC CAG AAC AAT GGA ACT CTC AAA GGA 4209  
lys ile ala ala ala phe lys phe val gln ser thr gln asn asn gly thr leu lys gly  
TCC AAT CCT TCC TGC CAG ACA TCA GGG CTC TTG GCA CAA TGG ATG CAC TCC ACT TCC AGG 4269  
ser asn pro ser cys gln thr ser gly leu leu ala gln trp met his ser asn ser arg  
CAT GAA GGC CAT AAG CAG CAC AGA TCA CAA ACT TTA CCT ATA ATT CGA GGC AAA AAT GCA 4329  
his glu gly his lys gln his arg ser gln thr leu pro ile ile arg gly lys asn ala  
CTT TCT AAC CCC AAA CTC TTA CAG ATG TTA GAC AAT ACC ATG ACC AGC AAC TCC AAT GAA 4389  
leu ser asn pro lys leu leu gln met leu asp asn thr met thr ser asn ser asn glu  
ATA GAC ATC GTG CAT CAT GTA GAC ACT GAG GCC AAT ATA GCT ACG GAG GGT TGC CTC ACT 4449  
ile asp ile val his his val asp thr glu ala asn ile ala thr glu gly cys leu thr  
ATT CTG GAC CTG GTA TCC CTC TTC ACA CAG ACT CAT CAG AGA CAA CTC CAA CAA TGT GAC 4509  
ile leu asp leu val ser leu phe thr gln thr his gln arg lys leu gln gln cys asp  
TGT CAA AAT TCA TTG ATG AAA AGG GGC TTT GAT ACC TAC ATG CTC TTT TTC CAA GTC AAT 4569  
cys gln asn ser leu met lys arg gly phe asp thr tyr met leu phe phe gln val asn  
CAG TCA GCC ACA GCG CTG AAG CAT GTG TTT GCC TCC TTG AGA CTG TTT GTA TGC AAG TTT 4629  
gln ser ala thr ala leu lys his val phe ala ser leu arg leu phe val cys lys phe  
CCT TCA GCG TTC TTT CAA GGG CCT GCT GAC CTC TGT GGA TCA TTC TGT TAC GAA GTC CTA 4689  
pro ser ala phe phe gln gly pro ala asp leu cys gly ser phe cys tyr glu val leu  
AAA TGC TGT AAC CAG AGG TCA CGG TCA ACT CAG ACA GAA GCC TCA GCC CTT CTG TAC TTG 4749  
lys cys cys asn his arg ser arg ser thr gln thr glu ala ser ala leu tyr leu  
TTC ATG AGG AAG AAT TTT GAA TTT AAC AAG CAG AAG TCA ATT GTC CGG TCC CAC TTA CAA 4809  
phe met arg lys asn phe glu phe asn lys gln lys ser ile val arg ser his leu gln  
CTC ATC AAA GCT GTG AGC CAG TCA CGG TCA ACT GAT GCT GGG ATT GGA GGC TCT CGG TTT CAA 4869  
leu ile lys ala val ser gln leu ile ala asp ala gly ile gly gly ser arg phe gln  
CAT TCG CTT GCA ATT ACC AAT AAT TTC GCC AAT GGA GAT AAG CAA ATG AAA AAC AGC AAT 4929  
his ser leu ala ile thr asn asn phe ala asn gly asp lys gln met lys asn ser asn

FIG 15/4

TTC CCA GCA GAG GTG AAG GAC CTG ACT AAG CGT ATA AGG ACT GTT TTG ATG GCC ACA GCT 4989  
 phe pro ala glu val lys asp leu thr lys arg ile arg thr val leu met ala thr ala  
 CAG ATG AAG GAG CAC GAG AAG GAC CCC GAG ATG CTG GTG GAT CTC CAG TAC AGC CTG GCA 5049  
 gln met lys glu his glu lys asp pro glu met leu val asp leu gln tyr ser leu ala  
 AAC TCC TAC GCA AGC ACT CCT GAA CTA CGC AGG ACC TGG CTG GAA AGT ATG GCC AAG ATT 5109  
 asn ser tyr ala ser thr pro glu leu arg arg thr trp leu glu ser met ala lys ile  
 CAT GCC AGA AAC GGA GAT TTA TCT GAG GCT GCC ATG TGT TAC ATC CAT ATT GCT GCT CTC 5169  
 his ala arg asn gly asp leu ser glu ala ala met cys tyr ile ala ala leu  
 ATT GCA GAG TAT CTG AAA AGA AAG GGT TAC TGG AAA GTG GAA AAG ATT TGC ACA GCA TCC 5229  
 ile ala glu tyr leu lys arg lys gly tyr trp lys val glu lys ile cys thr ala ser  
 CTG CTC TCG GAG GAT ACC CAC CCC TGT GAT AGC AAC TCA TTA CTA ACA ACT CCC AGT GGA 5289  
 leu leu ser glu asp thr his pro cys asp ser asn ser leu leu thr thr pro ser gly  
 GGA AGC ATG TTC TCT ATG GGA TGG CCA GCT TTT TTG AGC ATT ACA CCC AAC ATT AAG GAA 5349  
 gly ser met phe ser met gly trp pro ala phe leu ser ile thr pro asn ile lys glu  
 GAA GGA GCC GCG AAA GAG GAT TCT GGA ATG CAC GAT ACA CCC TAC AAT GAG AAT ATC CTG 5409  
 glu gly ala ala lys glu asp ser gly met his asp thr pro tyr asn glu asn ile leu  
 GTG GAG CAG CTA TAC ATG TGT GGG GAG TTT CTC TGG AAG TCT GAG CGA TAT GAA CTC ATT 5469  
 val glu gln leu tyr met cys gly glu phe leu trp lys ser glu arg tyr glu leu ile  
 GCT GAT GTC AAC AAG CCC ATC ATT GCT GTC TTT GAG AAA CAA CGA GAC TTC AAA AAA TTG 5529  
 ala asp val asn lys pro ile ile ala val phe glu lys gln arg phe lys lys leu  
 TCA GAT CTC TAC TAC GAC ATT CAT CGG TCA TAT CTG AAA GTG GCA GAG GTG GTG AAT TCG 5589  
 ser asp leu tyr tyr asp ile his arg ser tyr leu lys val ala glu val val asn ser  
 GAG AAG CGG CTG TTT GGT CGC TAC TAT CGT GTG GCA TTT TAT GGG CAG GGC TTT TTT GAA 5649  
 glu lys arg leu phe gly arg tyr tyr arg val ala phe tyr gly gln gly phe phe glu  
 GAA GAA GAA GGT AAA GAG TAT ATT TAT AAA GAG CCT AAG CTG ACA GGT CTG TCC GAG ATT 5709  
 glu glu glu gly lys glu tyr ile tyr lys glu pro lys leu thr gly leu ser glu ile  
 TCC CAA AGA TTA CTC AAG CTC TAT GCA GAT AAA TTT GGA GCA GAC AAT GTG AAG ATA ATC 5769  
 ser gln arg leu leu lys leu tyr ala asp lys phe gly ala asp val lys ile ile  
 CAG GAT TCC AAC AAG GTA AAC CCC AAG GAT TTG GAC CCC AAA TAT GCC TAC ATC CAG GTG 5829  
 gln asp ser asn lys val asn pro lys asp leu asp pro lys tyr ala tyr ile gln val  
 ACC TAT GTG ACG CGC TTC TTT GAG GAA AAG ATC GAA GAC CGG AAG ACA GAT TTC GAA 5889  
 thr tyr val thr pro phe phe glu glu lys glu ile glu asp arg lys thr asp phe glu  
 ATG CAC CAC AAC ATC AAC CGC TTT GTC TTC GAG ACA CCC TTC ACG CTG TCG GGC AAG AAG 5949  
 met his his asn ile asn arg phe val phe glu thr pro phe thr leu ser gly lys lys  
 CAC GGT GGG GTG GCG GAG CAG TGC AAG CGG CGG ACG ATC CTG ACA ACG AGT CAC CTG TTC 6009  
 his gly gly val ala glu gln cys lys arg arg thr ile leu thr thr ser his leu phe  
 CCC TAC GTG AAG AAG AGG ATC CAG GTC ATC AGC CAA TCA AGC ACA GAG CTG AAT CCT ATT 6069  
 pro tyr val lys lys arg ile gln val ile ser gln ser ser thr glu leu asn pro ile  
 GAA GTG GCA ATT GAC CAG ATG TCC AGG AAG GTC TCT GAG CTT AAT CAG CTT TGC ACA ATG 6129  
 glu val ala ile asp glu met ser arg lys val ser glu leu asn gln leu cys thr met  
 GAA GAA GTG GAC ATG ATC AGC CTA CAG CTC AAA CTG CAA GGA AGT GTC AGC GTG AAG GTT 6189  
 glu glu val asp met ile ser leu gln leu lys leu gln gly ser val ser val lys val

FIG 15/5

AAT GCT GGG CCA ATG GCC TAT GCA CGA GCT TTT CTT GAA GAA ACC AAT GCA AAG AAG TAC 6249  
asn ala gly pro met ala tyr ala arg ala phe leu glu glu thr asn ala lys lys tyr  
CCT GAC AAC CAA GTA AAG CTT TTG AAG GAG ATC TTC AGG CAA TTT GCA GAT GCA TGT GGG 6309  
pro asp asn gln val lys leu leu lys glu ile phe arg gln phe ala asp ala cys gly  
CAG GCC CTT GAC GTG AAT GAG CGC CTC ATC AAA GAG GAC CAG CTG GAG TAC CAG GAA GAA 6369  
gln ala leu asp val asn glu arg leu ile lys glu asp gln leu glu tyr gln glu glu  
CTG AGG TCC CAC TAC AAG GAC ATG CTC AGC GAA CTC TCC ACA GTC ATG AAT GAG CAG ATT 6429  
leu arg ser his tyr lys asp met leu ser glu leu ser thr val met asn glu gln ile  
ACG GGC AGG GAC GAC CTG TCA AAG CGC GGA GTG GAC CAA ACC TGC ACT CGA GTA ATT AGC 6489  
thr gly arg asp asp leu ser lys arg gly val asp gln thr cys thr arg val ile ser  
AAA GCA ACT CCG GCC CTA CCC ACG GTC TCC ATC TCA TCT AGT GCT GAA GTC TGA GAG GAA 6549  
lys ala thr pro ala leu pro thr val ser ile ser ser ser ala glu val OPA  
CCC TGG AGC ATC CGA TGC ACC TCT CAG AGA ACT CTC TAA ATG TTT TGC AGC TAA TCT CGG 6609  
GGA AGA AAA AGA TAG ATT TAA TTT ATT TGA AGT TTT TAC AGT GTT AAT CTT GTT TAC CTT 6669  
GCT AGC TTG GGA ATT TTG CCA GCC TCT GAA TTT GCA CAT TTT CTA TGA TTC CTT TGT TTC 6729  
CTT GAA GTA GTA TTG ATC AAG CCA CGC TAA ACA TTT GTT CTG AAA TTC CAA TGA ACG TGC 6789  
AGC TTA AAA GCA AAC TGA GTT TGC TCT TGG GTG TAA TTT GTT CAA TTC CAG GTC CTT GTA 6849  
CAC GCA TTT TAG AGG TCA AAG TGA ATG TTT TTA TAA CAT TTA AGC ATA TTT CCA ATG TAA 6909  
ATA GAA GAT TGT AAA ATA TAT GGT TTT TAT CAC ATT TCA AAG AAT GTT TTT AGT TGA TAC 6969  
TTA TGA AAG TAC CAA AAT TAT ATG GGT AAC GTT TCA GAT CTT ATA TTA AAA TAT TTG TGT 7029  
ATG TGT AAA AAC TGT TCG ATA AAT ACT AAT CTC TAA AGT TTG TGG ACT ACC TTT ATT TGT 7089  
AAT ATA TGT GCT TTT AAG AGC AAT GGG ATG TGA AAT TAC AAA AAG TAT TTT GCT GTT GAT 7149  
AAT ATG AAT ATG AAT AAA AAC  
7170

FIG 15/6



## A. Mouse CLASP-1 cDNA sequence

-169/1 -139/11  
 G CAC ACT GAC ATG GAC TGA AGG AGT AGA AAG CTA CAT AGA TGT AGC ATG AGC ACT TCC

-109/21 -79/31  
 CTT CTT AGG GGA GTG GAG AGA TTT GTT CAG CCA GCT CAG TGA AGC CTC AGA AAG AAA AGG

-49/41 -19/51  
 TTT AAG GAC CTC AGT AGT TTT CAA ATA TTT TAT GAC TCC ATT TCA AGG CAT ATG ATG AGC  
 met met ser

12/61 42/71  
 TTC CGA GGA AAG GAA TTC TGG AAG AGG AGG CGA ACA GTG AAG AGA GTG AAC CCA GAA GGA  
 phe arg gly lys glu phe trp lys arg arg arg thr val lys arg val asn pro glu gly  
 72/81 102/91  
 ATC CAC AAG GCT GGT GCT CAG GAA AAG CCC AGA CTC TTG GAT CCT TTG GAT TAT GAA ACC  
 ile his lys ala gly ala gln glu lys pro arg leu asp pro leu asp tyr glu thr  
 132/101 162/111  
 GTC ATT GAA GAA CTT GAA AAG ACC TAT CGG GAT GAT CCT CTT CAG GAC CTT CTG TTC TTC  
 val ile glu glu leu glu lys thr tyr arg asp asp pro leu gln asp leu leu phe phe  
 192/121 222/131  
 CCC AGT GAT GAC TTC TCA ACA GCC ACG GTT TCT TGG GAT ATC CGA ACA CTC TAT TCG ACG  
 pro ser asp asp phe ser thr ala thr val ser trp asp ile arg thr leu tyr ser thr  
 252/141 282/151  
 GTA CGA GAA GAG GCA GAG CAC AGG GCA GAA AGT CTG GTG AAA GAG GCT TGT AAA TTC  
 val pro glu glu ala glu his arg ala glu ser leu leu val lys glu ala cys lys phe  
 312/161 342/171  
 TAC AGT TCC CAG TGG TAC GTG GTA AAC TAC AAA TAT GAA CAA TAT TCT GGA GAC ATT CGA  
 tyr ser ser gln trp tyr val val asn tyr lys tyr glu gln tyr ser gly asp ile arg  
 372/181 402/191  
 CAG TTG CCC CGA GCA GAA CAC AAG CCA GAG AAA CTT CCT TCA CAT TCC TTT GAG GTT GAC  
 gln leu pro arg ala glu his lys pro glu lys leu pro ser his ser phe glu val asp  
 432/201 462/211  
 CAT GAA GAT GCT GAT AAG GAT GAA GAT ACC ACA TCC CAC TCA TCA TCC AAG GGC GGT GGG  
 his glu asp ala asp lys asp glu asp thr thr ser his ser ser ser lys gly gly gly  
 492/221 522/231  
 GGA GCT GGA GGT ACT GGT GTG TTC AAG TCT GGC TGG CTT TAC AAG GGG AAT TTT AAC AGC  
 gly ala gly gly thr gly val phe lys ser gly trp leu tyr lys gly asn phe asn ser  
 552/241 582/251  
 ACT GTG AAC AAT ACT GTC ACT GTT CGG TCA TTC AAA AAG CGC TAC TTC CAG CTG ACT CAG  
 thr val asn asn thr val thr val arg ser phe lys lys arg tyr phe gln leu thr gln  
 612/261 642/271  
 TTG CCT GAT AAC TCC TAC ATT ATG AAC TTT TAC AAA GAT GAA AAG ATA TCC AAA GAG CCC  
 leu pro asp asn ser tyr ile met asn phe tyr lys asp glu lys ile ser lys glu pro  
 672/281 702/291  
 AAG GGC TGC ATC TTT TTG GAT TCC TGC ACA GGT GTA GTA CAG AAT AAC AGG CTG AGG AAA  
 lys gly cys ile phe leu asp ser cys thr gly val val gln asn asn arg leu arg lys  
 732/301 762/311  
 TAT GCC TTC GAG TTG AAG ATG AAC GAC CTG ACC TAT TTT GTG CTG GCT GCT GAA ACA GAG  
 tyr ala phe glu leu lys met asn asp leu thr tyr phe val leu ala ala glu thr glu

792/321  
 TCA GAT ATG GAC GAA TGG ATC CAC ACA CTT AAC CGT ATC CTG CAG ATC AGT CCC GAG GGC  
 ser asp met asp glu trp ile his thr leu asn arg ile leu gln ile ser pro glu gly  
 852/341  
 CCA CTC CAG GGA AGG AAA AGT GCA GAG CTT GCT GAG CTG GGG CTA GAT CCA CTG GAT AAC  
 pro leu gln gly arg lys ser ala glu leu ala glu leu gly leu asp pro leu asp asn  
 912/361  
 TGC GTG ACT TGT GAA TGT ACA CTG GAG GAA ACC GAT TCT TCA GAG AAC AGC CTA CAT CCT  
 cys val thr cys glu cys thr leu glu glu thr asp ser ser glu asn ser leu his pro  
 972/381  
 GAC TTT GCA AAA TAC CTC ACA GAA ACC GAA GAC ACT GTC AAA ACA ACA CGA AAC ATG GGC  
 asp phe ala lys tyr leu thr glu thr glu asp thr val lys thr thr arg asn met gly  
 1032/401  
 AGA CTC AAT CTG TTC TCC CTG GAC CCA GAC ATA GAC ACC CTG AAG CTT CAA AAA AGG GAC  
 arg leu asn leu phe ser leu asp pro asp ile asp thr leu lys leu gln lys arg asp  
 1092/421  
 ATT TTT GAA AAT GAG TTG ATG ATC AAA CCC TTT GAA GAG AAA GCT GCC AAA AGA ATC ATG  
 ile phe glu asn glu leu met ile lys pro phe glu glu lys ala ala lys arg ile met  
 1152/441  
 ATC ATC TGT AGA GCT CTC AAC TTC AAT CTT CAG GGA TGT GTT ACA GAG AAT GAA TAT GAC  
 ile ile cys arg ala leu asn phe asn leu gln gly cys val thr glu asn glu tyr asp  
 1212/461  
 CCT GTA ACC AAT ATT GAG CCC TTT TTT GTG AGC GTG GCA CTT TAC GAC CTC AGA GAT AAC  
 pro val thr asn ile glu pro phe phe val ser val ala leu tyr asp leu arg asp asn  
 1272/481  
 AGG AAG ATC TCT GCG GAC TTC CAT GTG GAC CTA AAT CAC CCT GCT GTC CGG CAG ATG CTC  
 arg lys ile ser ala asp phe his val asp leu asn his pro ala val arg gln met leu  
 1332/501  
 TCG GGG ACC CCA CCG GCC TTG GAA AAC GGC AAT ATT GAC ACC GGT ACA CCA AGA CAA TCG  
 ser gly thr pro pro ala leu glu asn gly asn ile asp thr gly thr pro arg gln ser  
 1392/521  
 GAA GAA CCT CAC ATA AAG GGC CTT CCA GAG GAA TGG TTA AAA TTC CCA AAG CAG GCT GTC  
 glu glu pro his ile lys gly leu pro glu glu trp leu lys phe pro lys gln ala val  
 1452/541  
 TTC TCT GTG AGT GAT CCA CAC TCT GAA ATT GTT TTG GTG GCC AAA GTC GAA AAA GTC TTA  
 phe ser val ser asp pro his ser glu ile val leu val ala lys val glu lys val leu  
 1512/561  
 ATG GGA AAC ATC GGG AGT GGT GCT GAA CCT TAT ATC AAG AAT CCA GAC TCC AAC AAG TTT  
 met gly asn ile gly ser gly ala glu pro tyr ile lys asn pro asp ser asn lys phe  
 1572/581  
 GCA CAA AAG ATT CTA AAA TCC AAT AGG CAG TTC TGC AGC AAA TTG GGG AAA TAT CGG ATG  
 ala gln lys ile leu lys ser asn arg gln phe cys ser lys leu gly lys tyr arg met  
 1632/601  
 CCG TTT GCT TGG GCA GTG AGA TCT GTA TTT AAG GAC AAC CAG GGG AAC GTG GAC AGG GAC  
 pro phe ala trp ala val arg ser val phe lys asp asn gln gly asn val asp arg asp  
 1692/621  
 TCA CGG TTT TCA CCA CTG TAT AGA CAA GAA AGC AGC AAG ATG TCG TCT GAG GAC CTC CTA  
 ser arg phe ser pro leu tyr arg gln glu ser ser lys met ser ser glu asp leu leu  
 1752/641  
 AAA CTG GTG TCA GAC TAC AGA AGA GCT GAC CGG ATA AGC AAA ATG CAG AGC ATC CCT GGA  
 lys leu val ser asp tyr arg arg ala asp arg ile ser lys met gln ser ile pro gly  
 1812/661  
 AGC CTG GAT ATT GCT GTG GAC AAC ATT CCC TTG GAG CAC CCA AAC TGT GTA ACA TCG TCC  
 ser leu asp ile ala val asp asn ile pro leu glu his pro asn cys val thr ser ser

1872/681  
 TTT ATC CCT CTC AAG CCC TTC AAC GTG ACG GCT CAG TCA GAA CCT ACA GTG GAG GTG GAA  
 phe ile pro val lys pro phe asn val thr ala gln ser glu pro thr val glu val glu  
 1932/701  
 GAA TTT ATT TAT GAC TCA ACA AAG TAT TGC CGT CCA TAC CGA GTA TAC AAA AAT CAA ATT  
 glu phe ile tyr asp ser thr lys tyr cys arg pro tyr arg val tyr lys asn gln ile  
 1992/721  
 TAT GTA TAC CCC AAA CAC CTC AAA TAC GAT AGC CAG AAA TGC TTC AAC AAG GCA CGG AAT  
 tyr val tyr pro lys his leu lys tyr asp ser gln lys cys phe asn lys ala arg asn  
 2052/741  
 ATA ACT CTG TGC ATT GAA TTC AAA AAT TCA GAT GAC GAT GGA GCC AAG CCC ATG AAG TGT  
 ile thr val cys ile glu phe lys asn ser asp asp asp gly ala lys pro met lys cys  
 2112/761  
 ATT TAT GGG AAA CCT GGA GGG CCC CTC TTC ACT TCC TCT GCC TAC ACG GCT GTG CTA CAC  
 ile tyr gly lys pro gly gly pro leu phe thr ser ser ala tyr thr ala val leu his  
 2172/781  
 CAT TCT CAA AAT CCA GAT TTC TCT GAT GAG GTG AAA ATT GAA CTA CCA ACA CAA CTC CAT  
 his ser gln asn pro asp phe ser asp glu val lys ile glu leu pro thr gln leu his  
 2232/801  
 GGA AAA CAT CAC CTT TTG TTC TCC TTT TAC CAC ATC ACA TGT GAC ATC AAT GCC AAA GCC  
 gly lys his his leu leu phe ser phe tyr his ile thr cys asp ile asn ala lys ala  
 2292/821  
 AAT GCC AAA AAG AAA GAG GCT TTG GAG ACA TCA GTG GGC TAT GCA TGG CTT CCT CTG ATG  
 asn ala lys lys lys glu ala leu glu thr ser val gly tyr ala trp leu pro leu met  
 2352/841  
 AAA CAT GAT CAA ATA GCT TCT CAG GAG TAC AAC ATC CCA ATA GCA ACG ACC CTG CCT CCT  
 lys his asp gln ile ala ser gln glu tyr asn ile pro ile ala thr thr leu pro pro  
 2412/861  
 AAT TAT TTA AGC ATT CAA GAT CCT ACA AGT GCA AAG CAT GGT GGA AGT GAC ATT AAA TGG  
 asn tyr leu ser ile gln asp pro thr ser ala lys his gly gly ser asp ile lys trp  
 2472/881  
 GTC GAT GGT GGC AAA CCG CTT TTC AAA GTG TCC ACA TTT GTT GTA TCA ACA GTG AAC ACT  
 val asp gly gly lys pro leu phe lys val ser thr phe val val ser thr val asn thr  
 2532/901  
 CAG GAC CCA CAT GTA AAT GCA TTT TTC CGT CAG TGC CAA AAA AGA AAA GAC ATG TCT  
 gln asp pro his val asn ala phe phe arg gln cys gln lys arg glu lys asp met ser  
 2592/921  
 CAG TCA CCT ACC TCC AGC TTT GTC CGT GCC TGT AAG AAC TTA CTA AAT GTG GAC AAG ATC  
 gln ser pro thr ser ser phe val arg ala cys lys asn leu leu asn val asp lys ile  
 2652/941  
 CAC TCC ATC ATG AGT TTC CTG CCT ATC ATC TTG AAC CAG CTC TTC AAA ATT CTA GTG CAG  
 his ser ile met ser phe leu pro ile ile leu asn gln leu phe lys ile leu val gln  
 2712/961  
 AAC GAG GAA GAT GAA ATT ACT GCG ACC GTC ACC AGG GTT CTG GCT GAC ATT GTG GCC AAG  
 asn glu glu asp glu ile thr ala thr val thr arg val leu ala asp ile val ala lys  
 2772/981  
 TGT CAT GAG GAG CAA CTA GAC CAT TCT GTC CAG TCA TAC ATT AAG TTT GTA TTC AAG ACC  
 cys his glu glu gln leu asp his ser val gln ser tyr ile lys phe val phe lys thr  
 2832/1001  
 AAA TCC TAC AAA GAG AGA ACA ATA CAT GAG GAA CTG GCT AAA AAT TTG AGT GAT CTT TTG  
 lys ser tyr lys glu arg thr ile his glu glu leu ala lys asn leu ser asp leu leu  
 2892/1021  
 AAG TCC AAT GAC TCA ACG ATA GTC AAG CAT GTT CTA GAG CAT TCT TGG TTC TTC TTT GCC  
 lys ser asn asp ser thr ile val lys his val leu glu his ser trp phe phe ala  
 2952/1041  
 ATT ATT CTA AAA TCA ATG GCA CAG CAC TTG ATT GAC ACA AAC AAA ATT CAG CTT CCC AGA  
 ile ile leu lys ser met ala gln his leu ile asp thr asn lys ile gln leu pro arg

3012/1061  
 GCT CAA AGA TTC CCT GAG TCT TAC CAA AGC GAA CTA GAC AAC TTG GTG ATG GGC CTG TGT  
 ala gln arg phe pro glu ser tyr gln ser glu leu asp asn leu val met gly leu cys  
 3072/1081  
 GAC CAC GTG ATT TGG AAA TGC AAG GAA GCC CCT GAG GAA ACC AAA AGA GCA AAC CAC AGC  
 asp his val ile trp lys cys lys glu ala pro glu glu thr lys arg ala asn his ser  
 3132/1101  
 GTT GCC AGA TTC CTT AAG CGC TGC TTT ACA TTT ATG GAC CGG GGA TTC GTG TTT AAG ATG  
 val ala arg phe leu lys arg cys phe thr phe met asp arg gly phe val phe lys met  
 3192/1121  
 GTG AAC AAT TAC ATC AGC ATG TTC TCT TCT GGT GAG TTT AAG ACT TTA TGC CAG TAT AAG  
 val asn asn tyr ile ser met phe ser ser gly glu phe lys thr leu cys gln tyr lys  
 3252/1141  
 TTT GAT TTC CTT CAG GAA GTT TGT CAA CAT GAG CAC TTT ATC CCT TTG TGT CTC CCC ATA  
 phe asp phe leu gln glu val cys gln his glu his phe ile pro leu cys leu pro ile  
 3312/1161  
 AGA TCT GCA AAC ATT CCA GAT CCC TTG ACA CCT TCA GAA TCA ATC CGA GAG TTA CAT GCC  
 arg ser ala asn ile pro asp pro leu thr pro ser glu ser ile arg glu leu his ala  
 3372/1181  
 TCA GAT ATG CCT GAG TAC TCA GTC ACA AAT GAA TTT TGC CGC AAA CAC TTC TTA ATT GGA  
 ser asp met pro glu tyr ser val thr asn glu phe cys arg lys his phe leu ile gly  
 3432/1201  
 ATT CTT CTC CGA GAA GTT GGC TTT GCC CTG CAG GAG GAC CAA GAC ATC AGG CAC TTA GCT  
 ile leu leu val ile leu val gly phe ala leu gln glu asp gln asp ile arg his leu ala  
 3492/1221  
 TTA GCT CTC CTA AAA AAT CTA ATG GCT AAG CAC TCT TTC GAT GAT CGA TAC AGG GAA CCT  
 leu ala val leu lys asn leu met ala lys his ser phe asp asp arg tyr arg glu pro  
 3552/1241  
 AGG AAG CAG GCA CAG ATA GCG AGT CTG TAC ATG CCG CTC TAT GGT ATG CTC CTG GAC AAT  
 arg lys gln ala gln ile ala ser leu tyr met pro leu tyr gly met leu leu asp asn  
 3612/1261  
 ATG CCA AGA ATC TAC CTG AAG GAC CTG TAT CCT TTC ACC GTG AAC ACA TCC AAT CAG GGA  
 met pro arg ile tyr leu lys asp leu tyr pro phe thr val asn thr ser asn gln gly  
 3672/1281  
 TCT AGA GAT GAC CTC AGC ACT AAT GGA GGA TTT CAG ACT CAG ACG TCC ATG AAA CAT GCA  
 ser arg asp asp leu ser thr asn gly gly phe gln thr gln thr ser met lys his ala  
 3732/1301  
 ACT TCT GTG GAT ACA TCA TTT TCC AAA GAT GTT TTA AAT TCC ATA GCA GCA TTT TCA TCA  
 thr ser val asp thr ser phe ser lys asp val leu asn ser ile ala ala phe ser ser  
 3792/1321  
 ATA GCT ATT TCT ACA GTG AAC CAT GCA GAT TCC AGA GCG TCC TTA GCG AGC CTC GAC TCC  
 ile ala ile ser thr val asn his ala asp ser arg ala ser leu ala ser leu asp ser  
 3852/1341  
 AAC CCA AGT ACC ACA GAG AAG AGC AGT GAG AAG ACA GAC AAT TGT GAA AAG ATC CCA AGG  
 asn pro ser thr thr glu lys ser ser glu lys thr asp asn cys glu lys ile pro arg  
 3912/1361  
 CCC TTG TCT TTG ATT GGG TCA ACG CTT CGG TTT GAC AAA TTA GAT CAA GCA GAA ACC AGS  
 pro leu ser leu leu gly ser thr leu arg phe asp lys leu asp gln ala glu thr arg  
 3972/1381  
 AGT CTT CTT ATG TGT TTT CTT CAC ATT ATG AAG ACC ATT TCA GAT GAG ACT CTG ATT GCC  
 ser leu leu met cys phe leu his ile met lys thr ile ser asp glu thr leu ile ala  
 4032/1401  
 TAC TGC CAG AGA GCA CCC AGT CCA GAG GTG TCA GAC TTC TTC AGC ATC TTG GAC GTT TGT  
 tyr trp gln arg ala pro ser pro glu val ser asp phe phe ser ile leu asp val cys  
 4092/1421  
 CTT CAG AAT TTT AGA TAC CTA GGG AAA CGC AAT ATA ATA AGG AAA ATC GCT GCA GCG TTT  
 leu gln asn phe arg tyr leu gly lys arg asn ile ile arg lys ile ala ala ala phe

4152/1441  
 AAG TTT GTG CAG TCA ACC CAG AAC AAT GGG ACT CTG AAG GGA TCC AAT CCT TCC TGC CAG  
 lys phe val gln ser thr gln asn asn gly thr leu lys gly ser asn pro ser cys gln  
 4212/1461  
 ACA TCA GGT CTC TTG TCA CAA TGG ATG CAC ACA ACT TCT GGC CAC GAG GGA CAT AAG CAG  
 thr ser gly leu leu ser gln trp met his thr thr ser gly his glu gly his lys gln  
 4272/1481  
 CAC AGG TCT CAG ACT TTA OCT ATA ATC CGA GGC AAA AAT GCA CTT TCC AAC CCC AAA CTT  
 his arg ser gln thr leu pro ile ile arg gly lys asn ala leu ser asn pro lys leu  
 4332/1501  
 TTA CAG ATG TTG GAC AAC AGC ATG AAC AGC AAT TCC AAT GAA ATA GAC ATT GTC CAC CAT  
 leu gln met leu asp asn ser met asn ser asn ser asn glu ile asp ile val his his  
 4392/1521  
 GTT GAC ACA GAG GCC AAC ATA GCC ACC GAG GTC TGC CTC ACT ATT CTG GAC CTG CTG TCT  
 val asp thr glu ala asn ile ala thr glu val cys leu thr ile leu asp leu leu ser  
 4452/1541  
 CTC TTT ACC CAG GTC CAC CAG AGA CAG CTC CAA CAA TCC GAC TGT CAA AAT TCA CTC ATG  
 leu phe thr gln val his gln arg gln leu gln gln ser asp cys gln asn ser leu met  
 4512/1561  
 AAA AGG GTC TTC GAT ACT TAC ATG CTG TTT TTC CAA GTC AAC CAG TCA GCC TCA GCC CTG  
 lys arg val phe asp thr tyr met leu phe phe gln val asn gln ser ala ser ala leu  
 4572/1581  
 AAA CAC GTG TTT GCT TCT TTA AGA CTG TTT GTG TGC AAG TTT CCG TCA GCG TTT TTC CAA  
 lys his val phe ala ser leu arg leu phe val cys lys phe pro ser phe phe gln  
 4632/1601  
 GGG CCT GCT GAC CTC TGT GGC TCA TTC TGC TAT GAA GTC CTC AAA TGC TGT AAC CAC AGG  
 gly pro ala asp leu cys gly ser phe cys tyr glu val leu lys cys cys asn his arg  
 4692/1621  
 TCA AGG TTG ACT CAG ATG GAA GCT TCA GCA CTT CTA TAC TTC TTC ATG AGG AAG AAC TTT  
 ser arg leu thr gln met glu ala ser ala leu leu tyr phe phe met arg lys asn phe  
 4752/1641  
 GAG TTT AAC AAG CAG AAG TCA ATT GTC CGG TCT CAC TTA CAA CTC ATC AAA GCA GTG AGC  
 glu phe asn lys gln lys ser ile val arg ser his leu gln leu ile lys ala val ser  
 4812/1661  
 CAG TTA ATA GCT GAT GCG GGG ATC GGA GGG TCT CGC TTT CAA CAC TCC CTT GCA ATC ACG  
 gln leu ile ala asp ala gly ile gly gly ser arg phe gln his ser leu ala ile thr  
 4872/1681  
 AAC AAC TTT GCC AAT GGA GAT AAA CAG ATG AAA AAC AGC AAT TTC CCA GCA GAG GTG AAA  
 asn asn phe ala asn gly asp lys gln met lys asn ser asn phe pro ala glu val lys  
 4932/1701  
 GAT CTG ACT AAA CGC ATA AGG ACT GTT TTG ATG GCC ACA GCC CAG ATG AAG GAG CAT GAG  
 asp leu thr lys arg ile arg thr val leu met ala thr ala gln met lys glu his glu  
 4992/1721  
 AAG GAC CCA GAG ATG CTG GTG GAC CTT CAA TAC AGC CTA GCA AAC TCC TAT GCA AGT ACG  
 lys asp pro glu met leu val asp leu gln tyr ser leu ala asn ser tyr ala ser thr  
 5052/1741  
 CCG GAG TTA CGG AGG ACC TGG CTG GAA AGC ATG GCC AAG ATT CAT GCA AGA AAT GGA GAC  
 pro glu leu arg arg thr trp leu glu ser met ala lys ile his ala arg asn gly asp  
 5112/1761  
 CTG TCT GAG GCT GCG ATG TGT TAC ATC CAT ATA GCT GCA CTT ATT GCA GAA TAC CTG AAG  
 leu ser glu ala ala met cys tyr ile his ile ala ala leu ile ala glu tyr leu lys  
 5172/1781  
 CGC AAG GGT TAC TGG AAA ATG GAA AAG ATT TGC ACA CCA CCC CTG CTT CCA GAA GAC ACC  
 arg lys gly tyr trp lys met glu lys ile cys thr pro leu pro glu asp thr  
 5232/1801  
 CAA CCC TGT GAT AGC AAC TTA TTA CTA ACA ACT CCA GGC GGA GGA AGC ATG TTC TCT ATG  
 gln pro cys asp ser asn leu leu leu thr thr pro gly gly gly ser met phe ser met

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5292/1821  
GGA TGG CCA GGC TTT CTG AGC ATC ACC CCA  
gly trp pro ala phe leu ser ile thr pro  
5352/1841  
GAT TCT GGA ATG CAA GAC ACC CCG TAC AAT  
asp ser gly met gln asp thr pro tyr asn  
5412/1861  
TGT GTG GAG TTC CTT TGG AAG TCT GAA CGA  
cys val glu phe leu trp lys ser glu arg  
5472/1881  
ATC ATC GCT GTC TTT GAA AAG CAA CGA GAC  
ile ile ala val phe glu lys gln arg asp  
5532/1901  
ATC CAC CGG TCC TAT CTG AAA GTG GCA GAG  
ile his arg ser tyr leu lys val ala glu  
5592/1921  
CGT TAC TAT AGA GTG GCG TTT TAT GGG CAG  
arg tyr tyr arg val ala phe tyr gly gln  
5652/1941  
TAT ATC TAC AAA GAG CCT AAG CTG ACA GGG  
tyr ile tyr lys glu pro lys leu thr gly  
5712/1961  
CTC TAT GCA GAC AAA TTT GGA GCA GAC AAT  
leu tyr ala asp lys phe gly ala asp asn  
5772/1981  
AAC CCC AAG GAT CTG GAC CCC AAA TAT GCC  
asn pro lys asp leu asp pro lys tyr ala  
5832/2001  
TTT GAA GAA AAG GAA ATC GAG GAC CGA AAG  
phe glu glu lys glu ile glu asp arg lys  
5892/2021  
CGC TTT GTC TTT GAG ACA CCC TTC ACT CTG  
arg phe val phe glu thr pro phe thr leu  
5952/2041  
CAG TGC AAG CGG AGG ACA GTC CTG ACC ACA  
gln cys lys arg arg thr val leu thr thr  
6012/2061  
ATC CAG GTC ATC AGC CAA TCA AGC ACA GAG  
ile gln val ile ser gln ser ser thr glu  
6072/2081  
ATG TCC AGG AAG GTC TCT GAG CTT AAT CAG  
met ser arg lys val ser glu leu. asn gln  
6132/2101  
CGC CTA CAG CTC AAA CTC CAG GGC AGT GTC  
arg leu gln leu lys leu gln gly ser val  
6192/2121  
TAT GCT CGA GGC TTT CTT GAA GAA ACT AAT  
tyr ala arg ala phe leu glu glu thr asn  
6252/2141  
CTA CTA AAG GAA ATA TTC AGG CAA TTT GCA  
leu leu lys glu ile phe arg gln phe ala  
6312/2161  
GAG CGT CTC ATC AAG GAA GAC CAG CTG GAG  
glu arg leu ile lys glu asp gln leu glu  
6372/2181  
GAC ATG CTC AGT GAA CTG TCT GCC ATC ATG  
asp met leu ser glu leu ser ala ile met

5322/1831  
AAC ATT AAA GAA GAA GGA GCA ATG AAA GAG  
asn ile lys glu glu gly ala met lys glu  
5382/1851  
GAG AAC ATC CTG GTG GAA CAG CTG TAT ATG  
glu asn ile leu val glu gln leu tyr met  
5442/1871  
TAC GAA CTC ATC GCT GAT GTC AAT AAG CCC  
tyr glu leu ile ala asp val asn lys pro  
5502/1891  
TTC AAA AAA TTA TCA GAT CTC TAT TAT GAC  
phe lys lys leu ser asp leu tyr tyr asp  
5562/1911  
GTG GTG AAT TCG GAG AAG CGA TTG TTT GGT  
val val asn ser glu lys arg leu phe gly  
5622/1931  
GGA TTC TTT GAG GAG GAG GAA GGT AAA GAG  
gly phe phe glu glu glu gly lys glu  
5682/1951  
CTC TCG GAG ATC TCC CAA AGG CTT CTC AAG  
leu ser glu ile ser gln arg leu leu lys  
5742/1971  
GTG AAG ATA ATT CAA GAC TCC AAC AAG GTA  
val lys ile ile gln asp ser asn lys val  
5802/1991  
TAT ATT CAG GTG ACC TAT GTC ACA CCA TTC  
tyr ile gln val thr tyr val thr pro phe  
5862/2011  
ACA GAC TTT GAA ATG CAT CAC AAC ATC AAT  
thr asp phe glu met his his asn ile asn  
5922/2031  
TCA GGC AAG AAG CAC GGA GGA GTG GCT GAG  
ser gly lys lys his gly gly val ala glu  
5982/2051  
AGC CAC TTG TTC CCC TAC GTA AAG AAG AGG  
ser his leu phe pro tyr val lys lys arg  
6042/2071  
CTG AAT CCT ATC GAG GTG GCA ATT GAT GAG  
leu asn pro ile glu val ala ile asp glu  
6102/2091  
CTG TGC ACC ACA GAG GAG GTG GAT ATG ATC  
leu cys thr thr glu glu val asp met ile  
6162/2111  
AGC GTG AAG GTC AAT GCT GGG CCA ATT GCT  
ser val lys val asn ala gly pro met ala  
6222/2131  
GCA AAG AAG TAT CCT GAC AAC CAA GTT AAG  
ala lys lys tyr pro asp asn gln val lys  
6282/2151  
GAT GCG TGT GGG CAG GCT CTT GAT GTG AAT  
asp ala cys gly gln ala leu asp val asn  
6342/2171  
TAC CAG GAA GAA CTG AGG TCC CAT TAT AAG  
tyr gln glu glu leu arg ser his tyr lys  
6402/2191  
AAT GAG CAG ATT ACG GGC AGG GAC GAC CCA  
asn glu gln ile thr gly arg asp asp pro

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6432/2201	6462/2211
GCA AAG TGC GGA GTG GAG CGA CCC TAC ACC	ACA CGT GTA ACT AGC AAG GGG ACC GCG GCT
ala lys cys gly val glu arg pro tyr thr	thr arg val thr ser lys gly thr ala ala
6492/2221	6522/2231
GTA CCT GTG GTC TCC ATC TCA TCC AGT GCG	GAG GTT TGA GAG GAA CCC TGG AGC ATC CGA
val pro val val ser ile ser ser ala	glu val OFA
6552/2241	6582/2251
TGC ACC TCT CAG AGA ACT CTC TAA ATG TTT	TGC AGC TAA TCT CGG GGA AGA AAA AGA TAG
6612/2261	6642/2271
ATT TAA TTT ATT TGA AGT TTT TAC AGT GTT	AAT CTT GTT TAC CTT GCT AGC TTG GGA ATT
6672/2281	6702/2291
TTG CCA GCC TCT GAA TTT GCA CAT TTT CTA	TGA TTC CTT TGT TTC CTT GAA GTA GTA TTG
6732/2301	6762/2311
ATC AAG CCA CGC TAA ACA TTT GTT CTG AAA	TTC CAA TGA ACG TGC AGC TTA AAA GCA AAC
6792/2321	6822/2331
TGA GTT TGC TCT TGG GTG TAA TTT GTT CAA	TTC CAG GTC CTT GTA CAC GCA TTT TAG AGG
6852/2341	6882/2351
TCA AAG TGA ATG TTT TTA TAA CAT TTA AGC	ATA TTT CCA ATG TAA ATA GAA GAT TGT AAA
6912/2361	6942/2371
ATA TAT GGT TTT TAT CAC ATT TCA AAG AAT	GTT TTT AGT TGA TAC TTA TGA AAG TAC CAA
6972/2381	7002/2391
AAT TAT ATG GGT AAC GTT TCA GAT CTT ATA	TTA AAA TAT TTG TGT ATG TGT AAA AAC TGT
7032/2401	7062/2411
TGC ATA AAT ACT AAT CTC TAA AGT TTG TGG	ACT ACC TTT ATT TGT AAT ATA TGT GCT TTT
7092/2421	7122/2431
AAG AGC AAT GGG ATG TGA AAT TAC AAA AAG	TAT TTT GCT GTT GAT AAT ATG AAT ATG AAT
7152/2441	
AAA AAC	

B. Mouse CLASP-2 cDNA sequence

1/1	31/11
CCA CTC GAC TAT GAA AAT GTC ATC GTG CAG	AAG AAG ACG CAG ATC CTA AAC GAC TGC CTG
pro leu asp tyr glu asn val ile val gln	lys lys thr gln ile leu asn asp cys leu
61/21	91/31
CGG GAG <u>ATG</u> CTC CTC TTC CCT TAT GAT GAC	TTC CAG ACG GCC ATC CTG AGG CGG CAG GGG
arg glu met leu leu phe pro tyr asp asp	phe gln thr ala ile leu arg arg gln gly
121/41	151/51
CGG TAC TTA CGC TCC ACG GTC CCT GCA AAT	GCA GAG GAG GAA GCA CAG AGC CTG TTT GTC
arg tyr leu arg ser thr val pro ala asn	ala glu glu glu ala gln ser leu phe val
181/61	211/71
ACT GAG TGC ATC AAA ACC TAC AAC TCT GAC	TGG CAT CTT GTG ACC TAT AAA TAT GAA GAT
thr glu cys ile lys thr tyr asn ser asp	trp his leu val thr tyr lys tyr glu asp

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241/81  
TAC TCA GGA GAG TTC CGA CAG CTT CCA AAC AAA GTG CCC AAG CTG GAT AAA CTT CCG GTC  
tyr ser gly glu phe arg gln leu pro asn lys val pro lys leu asp lys leu pro val  
301/101  
CAC GTC TAT GAA GTC GAT GAG GAG GCC GAC AAA GAT GAG GAT GCT GCT TOC CTT GGG TCT  
his val tyr glu val asp glu glu ala asp lys asp glu asp ala ala ser leu gly ser  
361/121  
CAG AAG GGC GGG ATC ACC AAG CAT GGC TGG CTG TAC AAA GGC AAC ATG AAC AGT GCC ATC  
gln lys gly gly ile thr lys his gly trp leu tyr lys gly asn met asn ser ala ile  
421/141  
AGC GTG ACG ATG AGG TCA TTC AAG AGG CGG TTT TTC CAC CTG ATT CAA CTT GGC GAT GGA  
ser val thr met arg ser phe lys arg arg phe phe his leu ile gln leu gly asp gly  
481/161  
TCC TAT AAT CTA AAC TTT TAT AAA GAT GAG AAG ATC TCC AAG GAA CCG AAA GGG TCC ATA  
ser tyr asn leu asn phe tyr lys asp glu lys ile ser lys glu pro lys gly ser ile  
541/181  
TTC CTG GAT TCC TGC ATG GGT GTG ATC CAG AAC AAC AGA GTC AGG CGC TTC GCT TTT GAG  
phe leu asp ser cys met gly val ile gln asn asn arg val arg arg phe ala phe glu  
601/201  
CTC AAG ATG CAA GAC AAA AGC AGT TAC CTT CTG GCG GCA GAC AGC GAG GCA GAG ATG GAG  
leu lys met gln asp lys ser ser tyr leu leu ala ala asp ser glu ala glu met glu  
661/221  
GAG TGG GTC ACT GTT CTC AAC AAG ATC CTC CAG CTC AAC TTT GAA GCC GCA ATG CAA GAA  
glu trp val thr val leu asn lys ile leu gln leu asn phe glu ala ala met gln glu  
721/241  
AAG CGA AAC GGG GAC CCT CAT GAA GAT GAC GAG CAG AGC AAA CTG GAA GGT TCT GGT TCC  
lys arg asn gly asp pro his glu asp asp glu gln ser lys leu glu gly ser gly ser  
781/261  
GGT TTG GAC AGC TAC CTG CCT GAA CTT GCC AAG AGC ACC AGA GAA GCA GAG ATC AAA TTG  
gly leu asp ser tyr leu pro glu leu ala lys ser thr arg glu ala glu ile lys leu  
841/281  
AAA AGC GAG AGC AGA GTG AAG CTT TTT TAC TTG GAC CCA GAT ACC CAG AAA CTT GAC TTC  
lys ser glu ser arg val lys leu phe tyr leu asp pro asp thr gln lys leu asp phe  
901/301  
TCA TCC GCT GAA CCA GAA GTG AAG CCC TTT GAA GAA AAG TTT GGG AAA AGG ATT CTC GTC  
ser ser ala glu pro glu val lys pro phe glu glu lys phe gly lys arg ile leu val  
961/321  
AAG TGC AAC GAT TTG TCC TTT AAC CTG CAG TGC TGT GTC GCA GAG AAT GAG GAA GGA CCC  
lys cys asn asp leu ser phe asn leu gln cys cys val ala glu asn glu glu gly pro  
1021/341  
ACG ACA AAT GTC GAG CCT TTC TTT GTC ACC CTG TCC CTG TTC GAC ATA AAA TAC AAC CGA  
thr thr asn val glu pro phe phe val thr leu ser leu phe asp ile lys tyr asn arg  
1081/361  
AAG ATT TCT GCT GAC TTC CAC GTG GAC CTG AAC CAG TTC TCA GTG CGG CAG ATG CTG GCC  
lys ile ser ala asp phe his val asp leu asn his phe ser val arg gln met leu ala  
1141/381  
CCC ACG TCC CCA GCT CTG ATG AAC GGT GGC CAG AGC CCA CCT GCC TTC CAG GAT GCC CTT  
pro thr ser pro ala leu met asn gly gly gln ser pro pro ala phe gln asp ala leu  
1201/401  
CAT ACA GCC ATG CAG TAT CCG AAG CAG GGA ATA TTT TCA GTC ACG TGT CCT CAC CCA GAC  
his thr ala met gln tyr pro lys gln gly ile phe ser val thr cys pro his pro asp  
1261/421  
ATA TTT CTT GTG GCC AGA ATT GAG AAG GTC CTC CAA GGA AGC ATC ACG CAC TGT GCT GAA  
ile phe leu val ala arg ile glu lys val leu gln gly ser ile thr his cys ala glu  
1321/441  
CCG TAT ATG AGA AGC TCA GAC TCT TCT AAG CTT GCC CAG AAG GTG CTG AAG AAT GCC AAG  
pro tyr met arg ser ser asp ser ser lys val ala gln lys val leu lys asn ala lys



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1381/461  
CAG GCA TGC CAA AGA CTA GGA CAG TAC AGA  
gln ala cys gln arg leu gly gln tyr arg  
1441/481  
TTT AAA GAC ACC TCT GGA AAC CTG GAT AAA AAC GCC AGA TTT TCT GCC ATC TAC CGG CAA  
phe lys asp thr ser gly asn phe asp lys  
1501/501  
GAC AGC AAT AAG CTT TCA AAT GAT GAC ATG  
asp ser asn lys leu ser asn asp asp met  
1561/521  
GAG AAG ATG GCC AAA CTC CCA GTG ATT TTA  
glu lys met ala lys leu pro val ile leu  
1621/541  
TCC TGT GAC TTC CCT AAT TAT CTA AAT TCA TCA TAC ATT CCC ATG AGG CAA TTT GAA ACC  
ser cys asp phe pro asn tyr leu asn ser ser tyr ile pro met arg gln phe glu thr  
1681/561  
TGC AGT AAA TCT CCA ATC ACT TTT GAA GTA  
cys ser lys ser pro ile thr phe glu val  
1741/581  
ACC CAG CCT TAT ACA GTC TAC AGC AAT CAC  
thr gln pro tyr thr val tyr ser asn his  
1801/601  
GAC ACC CAG AAG TCG TTT GCC AAG GCC AGA  
asp ser gln lys ser phe ala lys ala arg  
1861/621  
TCT GAT GAA GAA GAC TCT CAA CCC TTG AAG  
ser asp glu glu asp ser gln pro leu lys  
1921/641  
TTC ACG AGA AGT GCC CTT GCC GCG GTC CTA  
phe thr arg ser ala leu ala ala val leu  
1981/661  
GAG ATC AAG ATA GAG CTG CCC GCC CAG CTG  
glu ile lys ile glu leu pro ala gln leu  
2041/681  
TTC CAC GTC AGC TGC GAT AAC TCC ACC AAA  
phe his val ser cys asp asn ser thr lys  
2101/701  
ACG CAG GTT GGC TTT TCC TGG CTG CCT CTC  
thr gln val gly phe ser trp leu pro leu  
2161/721  
CAG CAC ATC CCC GTC TCG GCT AAC CTG CCA  
gln his ile pro val ser ala asn leu pro  
2221/741  
ATG GGC AGG CAT TAT GGT CCA GAG GTT AAG  
met gly arg his tyr gly pro glu val lys  
2381/761  
ATC TCC ACT CAT CTG GTT TCC ACA GTG TAC  
ile ser thr his leu val ser thr val tyr  
2441/781  
CAA TAC TGT CAG AAA ACG GAA TCT GGA GCC  
gln tyr cys gln lys thr glu ser gly ala  
2501/801  
CTT AAG AGT CTG CAT GCG ATG GAA GGC CAT  
leu lys ser leu his ala met glu gly his  
2561/821  
AAT CAG CTA TTC AGA GTC CTC ACA AGA GCC  
asn gln leu phe arg val leu thr arg ala

1411/471  
ATG CCA TTC GCC TGG GCA GCA AGG ACG TTG  
met pro phe ala trp ala ala arg thr leu  
1471/491  
asn ala arg phe ser ala ile tyr arg gln  
1531/511  
CTC AAG CTG CTC GCA GAC TTC CGG AAA CCT  
leu lys leu leu ala asp phe arg lys pro  
1591/531  
GGC AAT CTA GAC ATT ACA ATT GAC AGT GTT  
gly asn leu asp ile thr ile asp ser val  
1651/551  
ser tyr ile pro met arg gln phe glu thr  
1711/571  
GAG GAG TTT GTG CCC TGC ATA CCC AAG CAC  
glu glu phe val pro cys ile pro lys his  
1771/591  
CTT TAT GTT TAC CCA AAA TAC TTG AAA TAT  
leu tyr val tyr pro lys tyr leu lys tyr  
1831/611  
AAC ATT GCT ATC TGC ATT GAG TTC AAG GAT  
asn ile ala ile cys ile glu phe lys asp  
1891/631  
TGC ATT TAC GCC AGA CCT GGT GGC CCG GTG  
cys ile tyr gly arg pro gly gly pro val  
1951/651  
CAC CAT CAG CAA AAC CCA GAA TTC TAC GAT  
his his gln gln asn pro glu phe tyr asp  
2011/671  
CAT GAG AGG CAC CAT TTA CTG TTC ACC TTC  
his glu arg his his leu leu phe thr phe  
2071/691  
GGA AGC ACG AAG AAG AAG GAC GCT GTG GAA  
gly ser thr lys lys lys asp ala val glu  
2131/711  
CTG AAA GAT GGA AGG GTG TTG ACG AGT GAG  
leu lys asp gly arg val leu thr ser glu  
2191/731  
TCT GGC TAC CTC GGC TAC CAG GAG CTC GGC  
ser gly tyr leu gly tyr gln glu leu gly  
2251/751  
TGG GTG GAA GGA GGC AAG CCA CTG TTG AAG  
trp val glu gly gly lys pro leu leu lys  
2311/771  
ACT CAG GAT CAA CAT TTA CAT AAT TTT TTC  
thr gln asp gln his leu his asn phe phe  
2371/791  
CAA GCC TCA GGG AGT GAA CTA GTA AAA TAC  
gln ala ser gly ser glu leu val lys tyr  
2431/811  
GTG ATG ATC GCC TTC TTG CCG ACC ATT TTA  
val met ile ala phe leu pro thr ile leu  
2491/831  
ACC CAG GAG GAG GTT GCT GTG AAC GTG ACA  
thr gln glu glu val ala val asn val thr

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2521/841  
CGG GTC ATT ATT CAT GTG GTT GCC CAG TGC  
arg val ile file his val val ala gln cys his glu glu gly leu glu ser his leu arg  
2581/861  
TCA TAT GTT AAG TTT GCC TAT AAG GCT GAG CCG TAC GTT GCA TCT GAG TAT AAG ACA GTG  
ser tyr val lys phe phe ala tyr lys ala glu pro tyr val ala ser glu tyr lys thr val  
2641/881  
CAC GAG GAA CTC AGC AAA TCC ATG ACC ACC ATT CTC AAG CCT TCT GCC GAT TTC CTT ACC  
his glu glu leu thr lys ser met thr thr ile leu lys pro ser ala asp phe leu thr  
2701/901  
AGC AAC AAA CTT CTG AAG TAC TCT TGG TTT TTC TTT GAT GTG CTG ATA AAG TCC ATG GCT  
ser asn lys leu leu lys tyr ser trp phe phe asp val leu ile lys ser met ala  
2761/921  
CAG CAT TTG ATT GAA AAT AAC AAA GTC AAG TTA CTG CCG AAC CAG AGA TTT CCG GCC TCC  
gln his leu ile glu asn asn lys val lys leu leu arg asn gln arg phe pro ala ser  
2821/941  
TAC CAT CAC GCT GTG GAA ACC GTG GTG AAC ATG CTG ATG CCA CAT ATC ACC CAG AAA TTT  
tyr his his ala val glu thr val val val asn met leu met pro his ile thr gln lys phe  
2881/961  
CGA GAT AAC CCA GAA GCA TCT AAA AAT GCC AAT CAC AGC CTC GCT GTG TTC ATC AAG AGA  
arg asp asn pro glu ala ser lys asn ala asn his ser leu ala val phe ile lys arg  
2941/981  
TGC TTC ACC TTC ATG GAC AGA GGC TTC GTC TTC AAG CAG ATC AAC AAC TAC ATC AGT TGC  
cys phe thr phe met asp arg gly phe val phe lys gln ile asn asn tyr ile ser cys  
3001/1001  
TTT GCT CCC GGG GAC CCC AAG ACT CTC TTT GAG TAC AAG TTT GAT TTT CTC CGC GTG GTG  
phe ala pro gly asp pro lys thr leu phe glu tyr lys phe glu phe leu arg val val  
3061/1021  
TGC AAC CAT GAA CAC TAT ATT CCT TTG AAT TTG CCG ATG CCA TTT GGA AAA GGA AGA ATT  
cys asn his glu his tyr ile pro leu asn leu pro met pro phe gly lys gly arg ile  
3121/1041  
CAG AGA TAC CAA GAT CTC CAG CTT GAC TAC TCC TTA ACA GAC GAG TTC TGC AGA AAC CAC  
gln arg tyr gln asp leu gln leu asp tyr ser leu thr asp glu phe cys arg asn his  
3181/1061  
TTC TTG GTG GGA CTG TTG CTA AGG GAG GTG GGC ACT GCG CTC CAG GAG TTC CCG GAG GTC  
phe leu val gly leu leu leu arg glu val gly thr ala leu gln glu phe arg glu val  
3241/1081  
CGA GTC ATC GCC ATC AGC ATG CTC AAG AAC CTG CTG ATA AAA CAT TCT TTT GAT GAC AGA  
arg val ile ala ile ser met leu lys asn leu leu ile lys his ser phe asp asp arg  
3301/1101  
TAC AAT TCG AGG AGT CAC CAG GCA AGG ATA GCC ACT CTC TAC CTG CCT CTG TTT GGT CTG  
tyr asn ser arg ser his gln ala arg ile ala thr leu tyr leu pro leu phe gly leu  
3361/1121  
CTT ATT GAA AAT GTC CAG CCG ATC AAC GTG AGG GAT GTG TCA CCC TTT CCT GTG AAC CCG  
leu ile glu asn val gln arg ile asn val arg asp val ser pro phe pro val asn pro  
3421/1141  
GGC AGT ATC GTG AAG GAC GAA GCC CTG GCT GTG CCT GCT GGG AAT CCA CTC ATG ACT CCG  
gly ser ile val lys asp glu ala leu ala val pro ala gly asn pro leu met thr pro  
3481/1161  
CAG AAG GGA AAC ACA CTT GAC CAC AGC CTG CAC AAA GAC CTC TTG GGC GGC ATC TCT GGC  
gln lys gly asn thr leu asp his ser leu his lys asp leu leu gly ala ile ser gly  
3541/1181  
ATT GCT TCT CCG TAT ACA GGC TCA ACC CCC AAC ATC AAC AGC GTG AGA AAT GCC GAC TCA  
ile ala ser pro tyr thr ala ser thr pro asn ile asn ser val arg asn ala asp thr  
3601/1201  
AGA GGC TCT CTC ATT AGC ACG GAC TCA GGG AAC AGC CTT CCA GAC AGG AAC CCC GAG AAG  
arg gly ser leu ile ser thr asp ser gly asn ser leu pro asp arg asn pro glu lys

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3661/1221  
AGC AAC TCT CTG GAT AAG CAG CAG AGT GGC  
ser asn ser leu asp lys gln gln ser gly  
3721/1241  
AAA CTG GAC CAG TCT GAG ATC AAG AGC CTG  
lys leu asp gln ser glu ile lys ser leu  
3781/1261  
ATG TCT GAC GAT GCC CTG TTT ACA TAT TGG  
met ser asp ala leu phe thr tyr trp  
3841/1281  
TTC TTT ACA ATA TCT GAG GTC TGC CTG CAC  
phe phe thr ile ser glu val cys leu his  
3901/1301  
GCC AGG AAC CAG GAG GGG TTG GGA CCC ATA  
ala arg asn gln glu gly leu gly pro ile  
3961/1321  
GTT TCC CGT AAC AGA ACA GGA ATG ATG CAT  
val ser arg asn arg thr gly met met his  
4021/1341  
AAC TCT CTC ACT TTT AAC CAC AGC TAC GGC  
asn ser val thr phe asn his ser tyr gly  
4081/1361  
CTT CTC GAA GCC AAC ATC GCT ACT GAG GTC  
leu leu glu ala asn ile ala thr glu val  
4141/1381  
TTC ACA CTG GCT TTT AAG AAC CAG CTC CTA  
phe thr leu ala phe lys asn gln leu leu  
4201/1401  
AAA GTT TTT GAC GTC TAC CTG TGT TTC CTT  
lys val phe asp val tyr leu cys phe leu  
4261/1421  
AAC GTC TTT ACT GCC TTA AGG TCT CTA ATT  
asn val phe thr ala leu arg ser leu ile  
4321/1441  
CGG GCG GAC ATG TGT GCC TCC CTG TGC TAT  
arg ala asp met cys ala ser leu cys tyr  
4381/1461  
AGT TCC ATT CGG ACG GAG GCC TCC CAG CTG  
ser ser ile arg thr glu ala ser gln leu  
4441/1481  
TAC ACA GGA AAG AAG TCT TTT GTT CGG ACG  
tyr thr gly lys lys ser phe val arg thr  
4501/1501  
CTG ATT GCA GAT GTG GTT GGC ATT GGA GGA  
leu ile ala asp val val gly ile gly gly  
4561/1521  
AAC AAC TGT GCC AAC AGC GAC CGG ATC ATC  
asn asn cys ala asn ser asp arg ile ile  
4621/1541  
GAT TTG ACT AAG AGG ATC CGC ACA GTC CTG  
asp leu thr lys arg ile arg thr val leu  
4681/1561  
AAC GAC CCG GAG ATG CTG GTC GAC CTC CAG  
asn asp pro glu met leu val asp leu gln  
4741/1581  
CCT GAG CTC AGG AAG ACG TGG CTA GAC AGT  
pro glu leu arg lys thr trp leu asp ser  
3691/1231  
ATG CTG GGA AAT TCC GTG GTT CGA TGC GAC  
met leu gly asn ser val val arg cys asp  
3751/1251  
CTG ATG TGT TTC CTC TAC GTG CTG AAA AGC  
leu met cys phe leu tyr val leu lys ser  
3811/1271  
AAC AAA GCT TCA ACT GCT GAA TTG ATG GAT  
asn lys ala ser thr ala glu leu met asp  
3871/1291  
CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA  
3931/1311  
GGT CAT GAT CGA AAG TCT GAG ACA TTG CCT  
gly his asp arg lys ser gln thr leu pro  
3991/1331  
GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT  
ala arg leu gln gln leu gly ser leu asp  
4051/1351  
CAG TCA GAG GCA GAT GTC GTT CAC CAG TCG  
his ser glu ala asp val val his gln ser  
4111/1371  
GCT CAT CAT GGG CAT AAT CCC CTC ATG AAG  
4171/1391  
ala asp his gly his asn pro leu met lys  
4231/1411  
CAA AAA CAC CAG TCA GAA ATG GCT TTA AAA  
gln lys his gln ser glu met ala leu lys  
4291/1431  
TAT AAG TTC CCC TCG GCG TTC TAC GAG GGG  
4351/1451  
GAG GTC CTC AAG TGC TGC AAC TCC AAG CTC  
glu val leu lys cys cys asn ser lys leu  
4411/1471  
CTC TAC TTC CTG ATG AGG AAC AAC TTC GAC  
leu tyr phe leu met arg asn asn phe asp  
4471/1491  
CAC TTA CAG GTC ATC ATC TCT GTC AGC CAA  
his leu gln val ile ile ser val ser gln  
4531/1511  
ACC AGA TTC CAG CAG TCC TTG TCT ATC ATC  
4591/1531  
thr arg phe gln gln ser leu ser ile ile  
4651/1551  
ATG GCC ACA GCC CAG ATG AAG GAG CAC GAG  
met ala thr ala gln met lys glu his glu  
4711/1571  
TAC AGC CTG GCT AAG TCC TAC GCC AGC ACC  
tyr ser leu ala lys ser tyr ala ser thr  
4771/1591  
AGT ATG GCG AGG ATT CAC GTT AAA AAT GGG GAC  
ser met ala arg ile his val lys asn gly asp

4801/1601  
 CTC TCA GAG GCG GCA ATG TGC TAT GTC CAC GTG ACA GCC TTG GTG GCA GAA TAT CTC ACA  
 leu ser glu ala ala met cys tyr val his val thr ala leu val ala glu tyr leu thr  
 4861/1621  
 CGG AAA GAA GCT GAC CTA GCA CTC CAG CGG GAA CCA CCT GCC TTC CCC TAC AGC CAT AGC  
 arg lys glu ala asp leu ala leu gln arg glu pro pro ala phe pro tyr ser his ser  
 4921/1641  
 ACC TGC CAG AGG AAG AGC TGG GGA GGC ATG TTC AGA CAG GGG TGC ACA GCC TTC AGG GTT  
 thr cys gln arg lys ser trp gly gly met phe arg gln gly cys thr ala phe arg val  
 4981/1661  
 ATC ACA CCA AAC ATC GAT GAA GAG GCT TCC ATG ATG GAA GAC GTC GGC ATG CAG GAC GTC  
 ile thr pro asn ile asp glu glu ala ser met met glu asp val gly met gln asp val  
 5041/1681  
 CAT TTC AAC GAG GAT GTG CTG ATG GAG CTG CTG GAG CAG TGT GCG GAT GGA CTT TGG AAG  
 his phe asn glu asp val leu met glu leu leu glu gln cys ala asp gly leu trp lys  
 5101/1701  
 CGC GAG CGC TAC GAG CTG ATC GCT GAC ATC TAT AAG CTC ATC ATC CCC ATC TAC GAA AAG  
 ala glu arg tyr glu leu ile ala asp ile tyr lys leu ile ile pro ile tyr glu lys  
 5161/1721  
 CGG AGG GAT TTC GAG AGA CTA GCC CAT CTG TAT GAC ACG CTG CAC CGC GCA TAC AGC AAA  
 arg arg asp phe glu arg leu ala his leu tyr asp thr leu his arg ala tyr ser lys  
 5221/1741  
 GTG ACA GAG GTC ATG CAC TCG GGC CGC AGG CTC CTG GGG ACC TAC TTC CGG GTG GCC TTC  
 val thr glu val met his ser gly arg arg leu leu gly thr tyr phe arg val ala phe  
 5281/1761  
 TTT GGA CAG GGG TTC TTC GAA GAC GAA GAT GGG AAG GAA TAC ATC TAC AAA GAG CCC AAG  
 phe gly gln gly phe phe glu asp glu asp gly lys glu tyr ile tyr lys glu pro lys  
 5341/1781  
 CTC ACG CCT CTG TCA GAG ATT TCT CAG AGA CTC CTT AAA CTT TAC TCG GAT AAA TTT GGT  
 leu thr pro leu ser glu ile ser gln arg leu leu lys leu tyr ser asp lys phe gly  
 5401/1801  
 TCC GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC CCG AAG GAT CTG GAC TCC  
 ser glu asn val lys met ile gln asp ser gly lys val asn pro lys asp leu asp ser  
 5461/1821  
 AAG TTT GCC TAC ATC CAG GTG ACC CAC GTG ACC CCA TTC TTT GAC GAA AAG GAG TTA CAA  
 lys phe ala tyr ile gln val thr his val thr pro phe phe asp glu lys glu leu gln  
 5521/1841  
 GAG AGG AGA ACA GAG TTT GAA CGA TGT CAC AAC ATC CGG CGC TTC ATG TTT GAG ATG CCC  
 glu arg arg thr glu phe glu arg cys his asn ile arg arg phe met phe glu met pro  
 5581/1861  
 TTC ACC CAG ACC GGG AAG AGG CAG GGT GGC GTG GAG GAG CAG TOT AAG CGG CGG ACC ATC  
 thr thr gln thr gly lys arg gln gly gly val glu glu gln cys lys arg arg thr ile  
 5641/1881  
 CTG ACA GCA ATA CAC TGC TTC CCC TAC GTG AAG AAG CGG ATC CCT GTC ATG TAC CAG CAC  
 leu thr ala ile his cys phe pro tyr val lys lys arg ile pro val met tyr gln his  
 5701/1901  
 CAC ACT GAC CTG AAG CCC ATT GAG GTG GCC ATC GAT GAA ATG AGC AAG AAG GTG GCC GAG  
 his thr ser leu asn pro ile glu val ala ile asp glu met ser lys lys val ala glu  
 5761/1921  
 CTC CGC CAG CTC TGC TCG TCG GCT GAA GTG GAT ATG ATC AAA CTG CAG CTC AAA CTG CAG  
 leu arg gln leu cys ser ser ala glu val asp met ile lys leu gln leu lys leu gln  
 5821/1941  
 GGC AGT GTG AGC GTC CAG GTC AAT GCT GGT CCG CTA GCA TAT GCC CGA GCC TTC CTC GAT  
 gly ser val ser val gln val asn ala gly pro leu ala tyr ala arg ala phe leu asp  
 5881/1961  
 GAC ACC AAC ACA AAA AGA TAC CCT GAC AAT AAG GTG AAA CTG CTG AAG GAA GTT TTC AGG  
 asp thr asn thr lys arg tyr pro asp asn lys val lys leu leu lys glu val phe arg

5941/1981  
 CAA TTT GTG GAA GCT TGT GGT CAA GCC TTG  
 gln phe val glu ala cys gly gln ala leu  
 6001/2001  
 CAA CTG GAG TAC CAG GAA GAG ATG AAG GCC AAC TAC AGG GAG ATG GCC AAG GAG CTC TCC  
 gln leu glu tyr gln glu glu met lys ala asn tyr arg glu met ala lys glu leu ser  
 6061/2021  
 GAC ATC ATG CGT GAG CAG ATT TGC CCC CTG  
 asp ile met arg glu gln ile cys pro leu  
 6121/2041  
 CTG CAC ATC TTC AAC GCC ATC AGC GGG ACA CCA ACA AGC ACA GTG GTT CAA GGG TTG ACC  
 leu his ile phe asn ala ile ser gly thr  
 6181/2061  
 AGC TCG TCC TCA GTT GTG TGA TTT TAC CTC ATG AAC CGT GTG TGG GGA CAT GCT TTG TCA  
 ser ser ser ser val val val  
 6241/2081  
 TGT GCA AAC TCA GGA TGA CTT CCA GAG CTA ATC ACT GGT GTG GCC AAG CAC AGG AAG AAG  
 6301/2101  
 CCA TGG GGA ATG GGA GAG AGA AGG AGC CTG  
 6361/2121  
 GAG TCG GGG GAA GGT GCA CAT AGT TTT TTA AAT CTC ACT GGC AAT ATT TAG TTT TCC TCA  
 6421/2141  
 TGT CTT AAC AGG TAT ATG TGG ATA CTC TTG

## C. Mouse CLASP-3 cDNA sequence

1/1  
 GTT TCA GCT GTG CCT GAA GAA AGT GAA ATG GAC CCA CAT GTT AGA GAT TGT ATA AGA AGT  
 val ser ala val pro glu glu ser glu met asp pro his val arg asp cys ile arg ser  
 61/21  
 TAC ACA GAA GAC TGG GCA GTT GTG GTC AGA AAA TAC CAT AAA CTG GGA ACA GGA TTT AAC  
 tyr thr glu asp trp ala val val val arg lys tyr his lys leu gly thr gly phe asn  
 121/41  
 CCC AAC ACA TTG GAT AAG CAG AAA GAA AGG CAA AAA GGA CTG CCC AGA CAA GTC TTT GAA  
 pro asn thr leu asp lys gln lys glu arg gln lys gly leu pro arg gln val phe glu  
 181/61  
 TCT GAT GAA GCT CCC GAT GGC AGC AGC TAC CAG GAT GAG CAA GAT GAT CTT AAA AGA CGT  
 ser asp glu ala pro asp gly ser ser tyr gln asp glu gln asp leu lys arg arg  
 241/81  
 TCG ATG TCA ATA GAT GAT ACT CCA AGG GGT AGC TGG GCC TGC AGT ATC TTT GAC TTA AAA  
 ser met ser ile asp asp thr pro arg gly ser trp ala cys ser ile phe asp leu lys  
 301/101  
 AAT TCA CTT CCT GAT GGC TTG CTT CCT AAT TTA CTT GAT CGA ACT CCA AAT GAA GAA ATA  
 asn ser leu pro asp ala leu leu pro asn leu leu asp arg thr pro asn glu glu ile  
 361/121  
 GAC CAT CAG AAT GAT GAC CAA AGG AAA TCA AAC GGC CAC AAG GAA CTG TTT GCT TTG CAT  
 asp his gln asn asp asp gln arg lys ser asn arg his lys glu leu phe ala leu his  
 421/141  
 CCA TCA CCA GAT GAG GAA GAA CCA ATC GAA AGG CTC AGT GTT CCT GAT GTG CCC AAA GAG  
 pro ser pro asp glu glu glu pro ile glu arg leu ser val pro asp val pro lys glu  
 481/161  
 CAT TTC GGA CAA AGA CTT CTT GTG AAA TGT TTA TCA CTC AAG TTT GAG ATT GAA ATT GAG  
 his phe gly gln arg leu leu val lys cys leu ser leu lys phe glu ile glu ile glu

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541/181  
CCC ATT TTT GCA AGT TTG GCT TTA TAT GAT 571/191  
pro ile phe ala ser leu ala leu tyr asp val lys glu lys lys lys ile ser glu asn  
601/201  
TTT TAT TTC GAC CTT AAT TCA GAG CAG ATG AAG GGA CTG TTA CGA CCG CAT GTG CCC CCT  
phe tyr phe asp leu asn ser glu gln met lys gly leu leu arg pro his val pro pro  
661/221  
GCT GCC ATC ACC ACT CTG GCA AGA TCA GCC ATT TTT TCT ATA ACT TAT CCT TCC CAA GAT  
ala ala ile thr thr leu ala arg ser ala ile phe ser ile thr tyr pro ser gln asp  
721/241  
GTC TTT CTT GTG ATA AAG TTA GAA AAA GTC CTT CAG CAA GGA GAC ATT GGA GAG TGT GCA  
val phe leu val ile lys leu glu lys val leu gln gln gly asp ile gly glu cys ala  
781/261  
GAA CCA TAT ATG ATT TTC AAA GAA GCT GAT GCC ACC AAG AAT AAG GAA AAA TTG GAG AAA  
glu pro tyr met ile phe lys glu ala asp ala thr lys asn lys glu lys leu glu lys  
841/281  
TTG AAA AGT CAA GCT GAC CAA TTT TGC CAG AGA CTT GGG AAA TAC CGC ATG CCT TTT GCT  
leu lys ser gln ala asp gln phe cys gln arg leu gly lys tyr arg met pro phe ala  
901/301  
TGG ACT GCG ATT CAT TTA ATG AAT ATT GTT AGC AGT GCT GGC AGC TTA GAA AGA GAC TCC  
trp thr ala ile his leu met asn ile val ser ser ala gly ser leu glu arg asp ser  
961/321  
ACA GAA GTC GAG ATC AGT ACT GGA GAA CGG AAA GGT TCT TGG TCA GAG AGG AGG AAT TCT  
thr glu gly glu ile ser thr gly glu arg lys gly ser trp ser glu arg arg asn ser  
1021/341  
AGT CTT GTT GGC AGG CGG TCC CTG GAG AGG ACG ACC AGT GGG GAT GAT GCT TGC AAC TTG  
ser leu val gly arg arg ser leu glu arg thr thr ser gly asp asp ala cys asn leu  
1081/361  
ACC AGC TTC TGG CCT GCC ACC CTC ACT GTG GCA AAC TTT TTT AAG CAG GAA GGA GAC CGT  
thr ser phe trp pro ala thr leu thr val ala asn phe phe lys gln glu gly asp arg  
1141/381  
TTA AGT GAT GAG GAC CTG TAC AAG TTC CTC GCT GAT ATG AGA AGG CCG TCT TCT GTC TTA  
leu ser asp glu asp leu tyr lys phe leu ala asp met arg arg pro ser ser val leu  
1201/401  
CGG AGG CTG AGA CCA ATT ACA GCT CAG CTG AAG ATA GAC ATT TCT CCT GCA CCT GAA AAT  
arg arg leu arg pro ile thr ala gln leu lys ile asp ile ser pro ala pro glu asn  
1261/421  
CCC CAT TAC TGC CTA ACC CCA GAG CTG CTT CAG GTG AAG CTG TAC CCC GAC AGC CGA GTC  
pro his tyr cys leu thr pro glu leu leu gln val lys leu tyr pro asp ser arg val  
1321/441  
AGG CCC ACC AGA GAA ATT TTA GAA TTT CCT GCC AGG GAT GTC TAT GTT CCA AAC ACA ACT  
arg pro thr arg glu ile leu glu phe pro ala arg asp val tyr val pro asn thr thr  
1381/461  
TAC AGA AAT CTT CTC TAC ATT TAC CTT CAA AGT CTT AAT TTT GCC AAC CGT CAA GGT TCT  
tyr arg asn leu leu tyr ile tyr pro gln ser leu asn phe ala asn arg gln gly ser  
1441/481  
GCC AGA AAC ATC ACA GTG AAA GTC CAG TTT ATG TAT GGG GAA GAC CCG AGC AAC GCA ATG  
ala arg asn ile thr val lys val gln phe met tyr gly glu asp pro ser asn ala met  
1501/501  
CGG GTA ATT TTT GGT AAA TCT AGC TGT TCA GAA TTT TCA AAG GAA GCC TAT ACA GCC GTA  
pro val ile phe gly lys ser ser cys ser glu phe ser lys glu ala tyr thr ala val  
1561/521  
GTA TAT CAT AAC AGG TCT CCT GAT TTT CAC GAG GAA ATC AAA GTC AAG CTC CCC GCC ACG  
val tyr his asn arg ser pro asp phe his glu glu ile lys val lys leu pro ala thr  
1621/541  
CTA ACT GAC CAC CAC CAC TTG CTC TTT ACT TTT TAT CAT GTT AGT TGC CAG CAG AAA CAA  
leu thr asp his his his leu leu phe thr phe tyr his val ser cys gln gln lys gln

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1681/561  
AAC ACT CCT CTC GAA ACC CCA GTC GGA TAT ACA TGG ATA CCA ATG CTG CAG AAT GGA CGG  
asn thr pro leu glu thr pro val gly tyr thr trp ile pro met leu gln asn gly arg  
1741/581  
TTG AAG ACA GGG CAG TTC TGC CTG CCA GTC TCC CTG GAA AAA CCA CGC GAG GCT TAT TCA  
leu lys thr gly gln phe cys leu pro val ser leu glu lys pro pro gln ala tyr ser  
1801/601  
GTG CTT TCC CCC GAG GTC CCT CTA CCT GGT ATG AAG TGG GTG GAC AAC CAC AAA GGA GTA  
val leu ser pro glu val pro leu pro gly met lys trp val asp asn his lys gly val  
1861/621  
TTT AAT GTT GAA GTT GTT GCT GTT TCA TCC ATT CAT ACA CAA GAC CCT TAT CTA GAC AAA  
phe asn val glu val val ala val ser ser ile his thr gln asp pro tyr leu asp lys  
1921/641  
TTC TTT GCT CTT GTC AAT GCT CTG GAT GAA CAC ATG TTC CCG GTC CGA ATT GGG GAC ATG  
phe phe ala leu val asn ala leu asp glu his met phe pro val arg ile gly asp met  
1981/661  
TGG ATC ATG GAA AAC AAC TTA GAG AGT GAA CTG AAG AGC AGC ATT TCA GCC TTG AAT TCC  
trp ile met glu asn asn leu glu ser glu leu lys ser ser ile ser ala leu asn ser  
2041/681  
TCA CAG CTG GAA CCC GTA GTC CGG TTT CTT CAT CTT CTG CTT GAT AAA CTC ATA CTT TTA  
ser gln leu glu pro val val arg phe leu his leu leu leu asp lys leu ile leu leu  
2101/701  
GTT GTT AGA CCA CCT GTG ATT GCT GGC CAA ATA GTT AAT CTA GGG CAA GCA TCT TTT GAA  
val val arg pro pro val ile ala gly gln ile val asn leu gly gln ala ser phe glu  
2161/721  
GCT ATG GCG TCA ATT ATA AAT CGA CTT CAC AAA AAC TTA GAA GGA AAT CAT GAC GAG CAT  
ala met ala ser ile ile asn arg leu his lys asn leu glu gly asn his asp gln his  
2221/741  
GGC AGA AAC AAC CTT CTC GCA TCG TAT ATC TAT TAT GTG TTC CGC CTG CCA AAT ACT TAC  
gly arg asn asn leu leu ala ser tyr ile tyr tyr val phe arg leu pro asn thr tyr  
2281/761  
CCT AAT TCA CCG TCA CCA GGT CCC GGG GGT TTG GGA GGA TCA GTG CAT TAT GCC ACA ATG  
pro asn ser pro ser pro gly pro gly gly leu gly gly ser val his tyr ala thr met  
2341/781  
GCT AGG TCT GCA GTG AGA CCT GCG AGC CTT AAC TTA AAT CCG TCT CGA AGC CTT AGC AAC  
ala arg ser ala val arg pro ala ser leu asn leu asn arg ser arg ser leu ser asn  
2401/801  
AGT AAC CCA GAT ATA TCT GGG ACT CCC ACA TCA CCA GAT GAT GAA GTT CCG TCA ATC ATT  
ser asn pro asp ile ser gly thr pro thr ser pro asp asp glu val arg ser ile ile  
2461/821  
GGC AGT AAG GCT AGT GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA AGT  
gly ser lys ala met asp arg ser cys asn arg met ser ser his thr glu thr ser ser  
2521/841  
TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG GCT  
phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu ala  
2581/861  
TTG CAG TGG GTC GTT TGC AGT GGC AGC GTT CCG GAG TCG GCT TTG CAG CAA GCC TGG TTC  
leu gln trp val val val cys ser gly ser val arg glu ser ala leu gln ala trp phe  
2641/881  
TTT TTT GAG TTG ATG GTA AAG AGC ATG GTG CAC CAC TTG TAC TTT AAT GAT AAG CTC GAC  
phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu asp  
2701/901  
GCT CCG AGG AAA AGT CGC TTT CCA GAA CGT TTT ATG GAT GAT ATT GCT GCC CTG GTT AGC  
ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val ser  
2761/921  
ACA ATT GCT GGC GAT GTC GTG TCG CGG TTT CAG AAG GAT ACA GAA ATG GTT GAG AGA CTC  
thr ile ala gly asp val val ser arg phe gln lys asp thr glu met val glu arg leu

2821/941  
 AAC ACA AGC CTT GCC TTC TTT CTC AAT GAC CTG CTG TCA GTT ATG GAC AGG GGG TTT GTT  
 asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe val  
 2881/961  
 TTT AGC CTC ATA AAG TCC TGC TAC AAA CAG GTA TCA GCA AAG CTG TAT TCA CTG CCA AAT  
 phe ser leu ile lys ser cys tyr lys gln val ser ala lys leu tyr ser leu pro asn  
 2941/981  
 CCA AGT GTC CTG GTG TCC CTG AGG TTG GAC TTT TTG CGA ATC ATC TGC AGC CAT GAG CAC  
 pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu his  
 3001/1001  
 TAT GTT ACA TTA AAC TTA CCC TGC AGC TTG CTC ACC CCG CCT GCA TCT CCA TCA CCT TCT  
 tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro ser  
 3061/1021  
 GTT TCT TCT GCA ACA TCT CAG AGC TCT GGA TTC TCC ACC AGT GTG CAG GAC CAG AAG ATT  
 val ser ser ala thr ser gln ser ser gly phe ser thr ser val gln asp gln lys ile  
 3121/1041  
 GCA AAC ATG TTC GAA TTG TCC TTA CCC TTC CGC CAG CAG CAT TAC CTG GCA GGC CTC GTG  
 ala asn met phe glu leu ser leu pro phe arg gln gln his tyr leu ala gly leu val  
 3181/1061  
 CTG ACT GAG CTT GCA CTC ATT CTA GAC CCT GAC GCT GAA GGA CTG TTT GGA TTG CAT AAG  
 leu thr glu leu ala leu ile leu asp pro asp ala glu gly leu phe gly leu his lys  
 3241/1081  
 AAA GTC ATC AAT ATG GTA CAC AAC TTA CTG TCC ACT CAC GAC TCT GAC CCA CGG TAC TCT  
 lys val ile asn met val his asn leu leu ser thr his asp ser pro arg tyr ser  
 3301/1101  
 GAC CCT CAG ATA AAA GCT CGG GTG GCT ATG TTG TAC CTA CCT CTT ATT GGT ATT ATC ATG  
 asp pro gln ile lys ala arg val ala met leu tyr leu pro leu ile gly ile ile met  
 3361/1121  
 GAA ACT GTA CCT CAA CTG TAT GAT TTT ACA GAA TCA CAC AAT CAA CGA GGA AGG CCA ATT  
 glu thr val pro gln leu tyr asp phe thr glu ser his asn gln arg gly arg pro ile  
 3421/1141  
 TGT ATA GCC CCT GAT GAC TAT GAC AGT GAG AGT GGG AGC ATG ATA AGC CAG ACG GTT GCC  
 cys ile ala pro asp asp tyr asp ser glu ser gly ser met ile ser gln thr val ala  
 3481/1161  
 ATG GCA ATT GCA GGA ACA TCC GTC CCT CAG CTG ACA AGA CCT GGC AGT TTT CTC CTC ACG  
 met ala ile ala gly thr ser val pro gln leu thr arg pro gly ser phe leu leu thr  
 3541/1181  
 TCA ACG AGT GGC CGG CAG CAC ACC ACC TTC TCA GCA GAG TCA AGC AGG AGC CTT TTG ATC  
 ser thr ser gly arg gln his thr thr phe ser ala glu ser ser arg ser leu leu ile  
 3601/1201  
 TGT CTG CTT TGG GTT CTC AAG AAT GCA GAT GAA ACG GTT CTG CAG AAA TGG TTT ACA GAT  
 cys leu leu trp val leu lys asn ala asp glu thr val leu gln lys trp phe thr asp  
 3661/1221  
 CTC TCA CTC CTC CAG CTG AAC CGG TTG TTA GAT CTG CTT TAC CTG TGT GTA TCT TGC TTT  
 leu ser val leu gln leu asn arg leu leu asp leu leu tyr leu cys val ser cys phe  
 3721/1241  
 GAG TAC AAA GGA AAA AAG GTA TTT GAA CGA ATG AAT AGT TTA ACT TTT AAG AAA TCA AAA  
 glu tyr lys gly lys lys val phe glu arg met asn ser leu thr phe lys lys ser lys  
 3781/1261  
 GAC ATG AGA GCC AAG CTT GAA GAA GCC ATT CTG GGG AGC ATC GGT GCC AGG CAG GAA ATG  
 asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu met  
 3841/1281  
 GTA CGG CGG AGC CGA GGG CAG CTC GAG AGG AGC CCA TCT GGA AGC GCC TTT GGG AGC CAA  
 val arg arg ser arg gly gln leu glu arg ser pro ser gly ser ala phe gly ser gln  
 3901/1301  
 GAA AAC CTG CGG TGG AGA AAG GAC ATG ACT CAC TGG CGT CAG AAC TCA GAG AAA CTC GAT  
 glu asn leu arg trp arg lys asp met thr his trp arg gln asn ser glu lys leu asp



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3961/1321  
AAG TCA AGA GCA GAG ATA GAA CAC GAA GCA  
lys ser arg ala glu ile glu his glu ala  
4021/1341  
AAC CTC ATC ATC TTA GAC ACG CTA GAG ATC  
asn leu ile ile leu asp thr leu glu ile  
4081/1361  
AAA GAG AGT ATC CTG GGT GGT GTG CTA AAA  
lys glu ser ile leu gly gly val leu lys  
4141/1381  
AGT GCA GTC TAT CTG CAG CAC TGC TTC GCC  
ser ala val tyr leu gln his cys phe ala  
4201/1401  
GAG CTC TTG TTT GAG GAA GAG ACA GAG CAG  
glu leu leu phe glu glu glu thr glu gln  
4261/1421  
CAT TGC AGT AGC AGC ATC AGT ACA ATC CGG  
his cys ser ser ser ile ser thr ile arg  
4321/1441  
ATG AGG CAG AAC TTT GAG ATC GGG AAT AAC  
met arg gln asn phe glu ile gly asn asn  
4381/1461  
TCA CTG TCC TCT TTG GTG GGT ACG TCT CAG  
ser leu ser ser leu val gly thr ser gln  
4441/1481  
CTA AAA ACT ATT TTG ACA TAT GCT GAA GAA  
leu lys thr ile leu thr tyr ala glu glu  
4501/1501  
GAT CAG GTC CAA GAT TTG GTC TTC AAT CTC  
asp gln val gln asp leu val phe asn leu  
4561/1521  
AAG GAG CAT CAG GAA GAC CCA GAA ATG CTG  
lys glu his gln glu asp pro glu met leu  
4621/1541  
TAC CAG ACG TCT CCA CAG CTC CGC CTG ACC  
tyr gln thr ser pro asp leu arg leu thr  
4681/1561  
GAA CGA ACG AAT CAT GCC GAA GCT GCT CAG  
glu arg ser asn his ala glu ala ala gln  
4741/1581  
GAG TAT CTG ACG ATG CTG GAA GAT CGG AAG  
glu tyr leu ser met leu glu asp arg lys  
4801/1601  
AAT ATT TCA TCT AAT GTA TTG GAA GAA TCT  
asn ile ser ser asn val leu glu glu ser  
4861/1621  
GAA GAA GGC ATT TGC TCT GGA AAG TAC TTC  
glu glu gly ile cys ser gly lys tyr phe  
4921/1641  
CAA GCG GCT GCT TCC TTC TCC ATG CGG GCG  
gln ala ala ala ser phe ser met ala gly  
4981/1661  
GTA CTC ATT OCT ATT CAT GAA GCT AAT CGG  
val leu ile pro ile his glu ala asn arg  
5041/1681  
AAA CTT CAG CAG GCA TTC AGC AAA ATC GTC  
lys leu gln glu ala phe ser lys ile val  
3991/1331  
CTG ATT GAT GGA AAC CTG GCT ACT GAA GCA  
leu ile asp gly asn leu ala thr glu ala  
4051/1351  
4111/1371  
GTG CTG CTA CAG AGC ATG GCC TGC AAC CAA  
val leu leu gln ser met ala cys asn gln  
4171/1391  
ACG CAG AGA GCC CTG GTC TCA AAG TTT CCT  
thr gln arg ala leu val ser lys phe pro  
4231/1411  
TGT GCG GAT CTG TGC CTC CGG CTT CTC CGT  
4291/1431  
TGC CAC GCT AGT GCC TCC CTT TAC CTC CTC  
ser his ala ser ala ser leu tyr leu leu  
4351/1451  
TTT GCC AGA GTG AAA ATG CAA GTG ACG ATG  
4411/1471  
GAT CTA GAA TTG AGG GAA ACC ACA TTT CCT  
asp leu glu leu arg glu thr thr phe pro  
4531/1511  
CAT ATC ATC CTT TCT GAC ACT GTT AAG ATG  
4591/1531  
ile asp leu met tyr arg ile ala lys gly  
4651/1551  
TGG TTG CAG AAC ATG GCT GGC AAG CAC TCT  
trp leu gln asn met ala gly lys his ser  
4711/1571  
cys leu val his ser ala ala leu val ala  
4771/1591  
TAT CTT CCT GTT GGA TGC GTA ACA TTC CAG  
4831/1611  
GCT GTC TCA GAT GAT GTG GTA TCT CCA GAT  
ala val ser asp asp val val ser pro asp  
4891/1631  
ACT GAA TCG GGA CTG GTG GGC TTA CTG GAA  
4951/1651  
ATG TAC GAA GCA GTT AAT GAG GTT TAC AAA  
met tyr glu ala val asn glu val tyr lys  
5011/1671  
GAT GCA AAG AAG CTC TCC ACA ATT CAT GGC  
5071/1691  
asp ala lys lys leu ser thr ile his gly  
5131/1711  
CAT CAG GAT GGT AAG CGG ATG TTT GGC ACC  
lys arg met phe gly thr

5101/1701  
 TAT TTC CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAG GAA TTT GTT  
 tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln glu phe val  
 5161/1721  
 TAC AAG GAG CCT GCA ATA ACC AAA CTC GCA GAG ATT TCT CAC AGA TTG GAG GGA TTT TAT  
 tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu gly phe tyr  
 521/1741  
 GGA GAA AGA TTT GGA GAG GAT GTG CTT GAA GTA ATC AAG GAC TCT AAT CCT GTA GAC AAG  
 gly glu arg phe gly glu asp val leu glu val ile lys asp ser asn pro val asp lys  
 5281/1761  
 TGC AAA TTA GAT CCA AAC AAG GCA TAT ATT CAG ATT ACC TAC GTG GAG CCC TTC TTT GAC  
 cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro phe phe asp  
 5341/1781  
 ACC TAT GAG ATG AAG GAC AGA ATC ACT TAT TTT GAC AAA AAT TAT AAT CTC CGG CGT TTC  
 thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu arg arg phe  
 5401/1801  
 ATG TAC TGC ACA CCC TTC ACT TTA GAT GGC CGT GCT CAT GGG GAG CTT CAT GAA CAA TTC  
 met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his glu gln phe  
 5461/1821  
 AAA CGG AAG ACC ATT CTG ACA ACG TCT CAT GCC TTT CCT TAC ATT AAA ACA AGA GTC AAT  
 lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr arg val asn  
 5521/1841  
 GTC ACT CAC AAA GAA GAG ATA ATC TTA ACA CCA ATT GAA GTT GGT ATC GAA GAC ATG CAG  
 val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu asp met gln  
 5581/1861  
 AAA AAG ACT CAG GAA TTG GCA TTT GCA ACA CAT CAG GAT CCA GCA GAC CCC AAA ATG CTT  
 lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro lys met leu  
 5641/1881  
 CAA ATG GTC CTC CAG GGG TCT GTA GGA ACA ACT GTA AAC CAG GGA CTT CTG GAG GTT GCC  
 gln met val leu gln gly ser val gly thr tht val asn gln gly pro leu glu val ala  
 5701/1901  
 CAG GTC TTC CTG TCT GAA ATA CCT GGT GAC CCG AAG CTC TTC AGA CAT CAC AAC AAG CTG  
 gln val phe leu ser glu ile pro gly asp pro lys leu phe arg his his asn lys leu  
 5761/1921  
 CGC CTT TGT TTC AAG GAC TTT ACT AAA AGG TGT GAG GAT GCC TTA CGA AAA AAT AAG AGC  
 arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys asn lys ser  
 5821/1941  
 TTA ATT GGA CCA GAT CAA AAG GAG TAT CAA AGA GAA CTG GAG AGA AAT TAC CAT CGC CTT  
 leu ile gly pro asp gln lys glu tyr gln arg glu leu glu arg asn tyr his arg leu  
 5881/1961  
 AAA GAG GCT CTG CAG CCA CTG ATA AAC AGA AAA ATC CCT CAG CTA TAC AAG GCT GTG TTG  
 lys glu ala leu gln pro leu ile asn arg lys ile pro gln leu tyr lys ala val leu  
 5941/1981  
 CCT GTC ACT TGC CAC AGA GAT TCC TTC AGC CGA ATG AGC CTT CGA AAA ATG GAA CTC TAA  
 pro val thr cys his arg asp ser phe ser arg met ser leu arg lys met glu leu OCH  
 6001/2001  
 AAT ACA CAC TTG TTC TAT TCA TTT GAA AAG AAC CAT GTA TTC AAC ACT GAG TGT GAG GTC  
  
 6061/2021  
 TAT TGA AAA ATA GGA CTT GGA TGT CAT TCT GGA AGC AAT AGT ATC GAT TTA CTC TCT GAA  
  
 6121/2041  
 GAA TGT GCT CCC AGA TGC AGG CTG TTA CGT GTG AGG CTT GTG GCG TGG TTT CTA ACC TTC  
  
 6181/2061  
 TGG TAA CAT GCT GTC ATC TTA AAA ACA AAA GGT TTT AAT GAT TCA

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D. Mouse CLASP-4 cDNA sequence

-150

AGAGAAAGAGCGCGGGAGCTGGGCGCGGGCGCGAGCTGAGATGTGGCGGGCGGTCGGCGGTGTAACACAGCGCAGC  
AGCAGCAGCAGCGCGCGGGCGCGGGCGCGAGCTGAGCGCTCCGCGCGAGACCTCGCCGCACTCTGCC -1

1/1	31/11
ATG GCC GAA GTG CGC AAA TTC ACC AAG CGG	CTG AGC AAG CCA GGC ACG GCA GCC GAG CTC
Met ala glu val arg lys phe thr lys arg	leu ser lys pro gly thr ala ala glu leu
61/21	91/31
CGC CAG AGC GTG TCG GAG GCC GTG CGG GGC	TCC GTG GTG CTG GAA AAG GCC AAG TTA GTT
arg gln ser val ser glu ala val arg gly	ser val val leu glu lys ala lys leu val
121/41	151/51
GAA CCC CTG GAC TAT GAA AAT GTT ATC ACT	CAA CGG AAA ACC CAG ATC TAC AGT GAT CCC
glu pro leu asp tyr glu asn val ile thr	gln arg lys thr gln ile tyr ser asp pro
181/61	211/71
CTC AGA GAT CTG CTT ATG TTC CCC ATG GAA	GAC ATA TCT ATC TCA GTG ATT GGT CGT CAG
leu arg asp leu leu met phe pro met glu	asp ile ser ile ser val ile gly arg gln
241/81	271/91
CGC AGA ACA GTG CAG TCT ACT GTA CCA GAG	GAT GCT GAA AAG AGG GCC CAG AGT TTA TTT
arg arg thr val gln ser thr val pro glu	asp ala glu lys arg ala gln ser leu phe
301/101	331/111
GTC AAA GAG TGT ATT AAG ACC TAC AGC ACA	GAT TGG CAT GTG GTG AAC TAT AAG TAT GAG
val lys glu cys ile lys thr tyr ser thr	asp trp his val val asn tyr lys tyr glu
361/121	391/131
GAT TTC TCT GGG GAC TTT CGG ATG TTG CCA	TGC AAG TCT TTG AGA CCT GAA AAG ATT CCT
asp phe ser gly asp phe arg met leu pro	cys lys ser leu arg pro glu lys ile pro
421/141	451/151
AAT CAT GTG TTT GAG ATT GAT GAA GAT TGC	GAG AAA GAT GAG GAT TCA TCT TCT TTA TGT
asn his val phe glu ile asp glu asp cys	glu lys asp glu asp ser ser ser leu cys
481/161	511/171
TCT CAG AAG GGT GGT GTG ATA AAA CAA GGT	TGG TTG CAT AAA GCA AAT GTA AAT AGC ACC
ser gln lys gly gly val ile lys gln gly	trp leu his lys ala asn val asn ser thr
541/181	571/191
ATC ACA GTA ACC ATG AAG GTG TTC AAG AGA	CGG TAT TTT TAT TTG ACT CAA CTT CCT GAT
ile thr val thr met lys val phe lys arg	arg tyr phe tyr leu thr gln leu pro asp
601/201	631/211
GGT TCA TAT ATT CTC AAT TCT TAT AAA GAT	GAG AAA AAT TCC AAA GAG TCT AAA GGT TGC
gly ser tyr ile leu asn ser tyr lys asp	glu lys asn ser lys glu ser lys gly cys
661/221	691/231
ATC TAC TTG GAT GCC TGC ATT GAT GTT GTT	CAG TGC CCC AAA ATG CGC CGT CAT GCT TTT
ile tyr leu asp ala cys ile asp val val	gln cys pro lys met arg arg his ala phe
721/241	751/251
GAA CTC AAG ATG TTA GAT AAG TAT AGC CAT	TAT CTG GCA GCT GAA ACG GAG CAG GAA ATG
glu leu lys met leu asp lys tyr ser his	tyr leu ala ala glu thr glu gln glu met
781/261	811/271
GAG GAA TGG TTG ATA ATG TTG AAA AAG ATT	ATT CAG ATC AAT ACT GAC AGT TTA GTG CAA
glu glu trp leu ile met leu lys lys ile	ile gln ile asn thr asp ser leu val gln
841/281	871/291
GAG AAA AAG GAC ACA GTC GAG GCA ATA CAA	GAG GAG GAA ACT AGC AGC CAA GGA AAA GCC
glu lys lys asp thr val glu ala ile gln	glu glu glu thr ser ser gln gly lys ala
901/301	931/311
GAG AAC ATC ATG GCC ACT TTG GAA AGG AGC	ATC CAT CCG GAA CTG ATG AAG TAT CGC AGA
glu asn ile met ala ser leu glu arg ser	met his pro glu leu met lys tyr gly arg

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961/321  
GAA ACA GAA CAA CTG AAC AAA CTC AGT AGA GGA GAC GGA AGA CAG AAT CTC TTT TCT TTC  
glu thr glu gln leu asn lys leu ser arg gly asp gly arg gln asn leu phe ser phe  
1021/341  
GAC TCA GAG GTT CAG AGA TTA GAC TTT TCA GGA ATT GAG CCT GAT GTA AAG CCA TTT GAA  
asp ser glu val gln arg leu asp phe ser gly ile glu pro asp val lys pro phe glu  
1081/361  
GAA AAG TGC AAC AAG CGT TTC ATG GTG AAT TGC CAT GAT TTA ACT TTC AAT ATC TTG GGT  
glu lys cys asn lys arg phe met val asn cys his asp leu thr phe asn ile leu gly  
1141/381  
CAC ATT GGA GAC AAT GCA AAA GGA CCA CCC ACA AAT GTT GAG CCC TTT TTC ATC AAC CTC  
his ile gly asp asn ala lys gly pro pro thr asn val glu pro phe phe ile asn leu  
1201/401  
GCC TTA TTT GAT GTA AAG AAC AAT TGT AAA ATT TCA GCA GAC TTT CAT GTA GAT TTG AAC  
ala leu phe asp val lys asn asn cys lys ile ser ala asp phe his val asp leu asn  
1261/421  
CCA CCC TCT GTC CGT GAA ATG CTG TGG GGT ACC TCG ACC CAA CTG TCC AAT GAT GGG AAT  
pro pro ser val arg glu met leu trp gly thr ser thr gln leu ser asn asp gly asn  
1321/441  
GCA AAG GGC TTT TCA CCT GAG TCT CTC ATC CAT GGA ATT GCT GAG TCT CAG TTA TGC TAC  
ala lys gly phe ser pro glu ser leu ile his gly ile ala glu ser gln leu cys tyr  
1381/461  
ATA AAG CAG GGA ATC TTC TCA GTG ACG AAC CCA CAT CCT GAA ATT TTC CTA GTT GTG AGA  
ile lys gln gly ile phe ser val thr asn pro his pro glu ile phe leu val val arg  
1441/481  
ATT GAA AAG GTG CTG CAG GGA AAC ATC ACA CAC TGT GCA GAA CCC TAC ATC AAA AAC TCA  
ile glu lys val leu gln gly asn ile thr his cys ala glu pro tyr ile lys asn ser  
1501/501  
GAT CCG ATA AAG ACA GCC CAG AAG GTA CAC AGG ACA GCT AAA CAA GTG TGT AGT CGC CTT  
asp pro ile lys thr ala gln lys val his arg thr ala lys gln val cys ser arg leu  
1561/521  
GGA CAA TAC AGA ATG CCA TTT GCT TGG GCA GCC AGA CCC ATT TTC AAA GAT GTT CAG GGC  
gly gln tyr arg met pro phe ala trp ala ala arg pro ile phe lys asp val gln gly  
1621/541  
TCT CTG GAT CTG GAT GGG AGA TTT TCC CCT TTG TAT AAA CAA GAC AGT AGC AAG CTT TCA  
ser leu asp leu asp gly arg phe ser pro leu tyr lys gln asp ser ser lys leu ser  
1681/561  
AAT GAA GAT ATT CTC AAG TTG CTC TCA GAA TAC AAA AAG CCA GAG AAG ACA AAA TTG CAG  
asn glu asp ile leu lys leu leu ser glu tyr lys lys pro glu lys thr lys leu gln  
1741/581  
ATT ATC CCT GGA CAG CTG AGT ATC ACA GTG GAA TGT GTT CCT GTA GAT TTA CCA AAT TGT  
ile ile pro gly gln leu ser ile thr val glu cys val pro val asp leu pro asn cys  
1801/601  
ATT ACC TCT TCA TAT GTG CCC CTG AAG CCT TTT GAA AAG AAT TGT CAG AAT ATT ACT GTG  
ile thr ser ser tyr val pro leu lys pro phe glu lys asn cys gln asn ile thr val  
1861/621  
GAG GTT GAA GAG TTT GTT CCA GAA ATG ACA AAA TAT TGT TAT CCA TTC ACT ATT TAC AAA  
glu val glu glu phe val pro glu met thr lys tyr cys tyr pro phe thr ile tyr lys  
1921/641  
AAT CAT CTG TAT GTA TAT CCC TTG CAA TTA AAA TAT GAC AGC CAG AAA TCG TTT GCC AAG  
asn his leu tyr val tyr pro leu gln leu lys tyr asp ser gln lys ser phe ala lys  
1981/661  
GCT AGC AAC ATT GCT GTC TGT GTG GAA TTC CGG GAT TCG GAT GAA AGT GAC GCG TCT GCG  
ala arg asn ile ala val cys val glu phe arg asp ser asp glu ser asp ala ser ala  
2041/681  
CTA AAG TGC ATT TAC GGA AAA CCA GCA GGG TCT GTT TTT ACC ACA AAT GCT TAT GCT GTG  
leu lys cys ile tyr gly lys pro ala gly ser val phe thr thr asn ala tyr ala val

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2101/701  
 GTC TCG CAT CAC AAC CAA AAT CCG GAG TTC  
 val ser his his asn gln asn pro glu phe  
 2161/721  
 CAC CTG CAG CAG AAG CAT CAC CTG CTT TTT  
 his leu his gln lys his his leu leu phe  
 2221/741  
 ACA AAA GGA ACA ACC AAA AAG CAA GAC ACA  
 thr lys gly thr thr lys lys gln asp thr  
 2281/761  
 CCT TTG CTG AAG GAT GGG AGG GTC ATC ACA  
 pro leu leu lys asp gly arg val ile thr  
 2341/781  
 CTT CCT CCA GGC TAC TTG AAT GTG AAT GAT  
 leu pro pro gly tyr leu asn val asn asp  
 2401/801  
 ATC AAG TGG GTA GAT GGT GCA AAG CCT TTG  
 ile lys trp val asp gly ala lys pro leu  
 2461/821  
 ATT TAT ACT CAG GAT CTG CAT GTG CAC AAA  
 ile tyr thr gln asp leu his val his lys  
 2521/841  
 GGC TCA AAA GAA GTT CCA GGG GAA CTC ATT  
 cys ser lys gly val pro gly glu leu ile  
 2581/861  
 ATC CAA GTC ATG ATA CAG TTT CTA CCT GTA  
 ile gln val met ile gln phe leu pro val  
 2641/881  
 AAC ATG ACC CAT GAA GAT GAC GTT CCC ATC  
 asn met thr his glu asp asp val pro ile  
 2701/901  
 TCT AAG TGT CAT GAA GAA GGC TTG GAG AGC  
 ser lys cys his glu glu gly leu glu ser  
 2761/921  
 AGA CCT GAA AAA CCA AGC ACT CTT CAG GCC  
 arg pro glu lys pro ser thr leu gln ala  
 2821/941  
 ATG ATA GCA ATA TTG AAA CAG TCT GCA GAT  
 met ile ala ile leu lys gln ser ala asp  
 2881/961  
 TCA TGG TTT TTC TTT GAA ATA ATT GCA AAG  
 ser trp phe phe glu ile ile ala lys  
 2941/981  
 AAA ATT AAG CTC CCC AGG GGC CAA AGG TTT  
 lys ile lys leu pro arg gly gln arg phe  
 3001/1001  
 CTG CTC CTT GCA ATA ATT CCC CAT GTG ACC  
 leu leu leu ala ile ile pro his val thr  
 3061/1021  
 CGA AAT GGG AAT TAT AGC TTA GCC AGC TTT  
 arg asn gly asn tyr ser leu ala ser phe  
 3121/1041  
 GGA TTT GTT TTC AAT TTG ATA AAT GAC TAT  
 gly phe val phe asn leu ile asn asp tyr  
 3181/1061  
 GTT CTT GCT GAA TAC AAG TTT GAA TTT CTC  
 val leu ala glu tyr lys phe glu phe leu  
 2131/711  
 TAT GAT GAG ATC AAA ATT GAG CTT CCC ATT  
 tyr asp glu ile lys ile glu leu pro ile  
 2191/731  
 TTT ACT TTT TAT CAT GTG AGT TGT GAA ATC AAC  
 thr phe tyr his val ser cys glu ile asn  
 2251/751  
 GTG GAA ACT CCA GTG GGA TTT GCC TGG GTA  
 val glu thr pro val gly phe ala trp val  
 2311/771  
 TTG GAG CAG CAG CTG CCA GTC TCA GCC AAT  
 leu glu gln gln leu pro val ser ala asn  
 2371/791  
 GCT GAA TCA AGA AGG CAA TCA AAT GCG GAT  
 ala glu ser arg arg gln ser asn ala asp  
 2431/811  
 CTG AAG ATT AAG ACC CAC TTA GAA TCA ACC  
 leu lys ile lys thr his leu glu ser thr  
 2491/831  
 TTC TTC CAT CAT TGC CAG CTG ATT CAG TCG  
 phe phe his his cys gln leu ile gln ser  
 2551/851  
 AAA TAT TTA AAG TGT TTG CAT GCC ATG GAG  
 lys tyr leu lys cys leu his ala met glu  
 2611/871  
 ATT CTT ATG CAA CTC TTC CGA GTT CTC ACA  
 ile leu met gln leu phe arg val leu thr  
 2671/891  
 AAC TGC ACC ATG GTT CTC TTA CAC ATT GTG  
 asn cys thr met val leu leu his ile val  
 2731/911  
 TAC TTA AGA TCC TTC ATA AAG TAT AGC TTC  
 tyr leu arg ser phe ile lys tyr ser phe  
 2791/931  
 CAG TTG ATA CAT GAA ACC CTG GCT ACG ACT  
 gln leu ile his glu thr leu ala thr thr  
 2851/951  
 TTC CTA GCC ATA AAT AAA CTT CTA AAG TAC  
 phe leu ala ile asn lys leu leu lys tyr  
 2911/971  
 TCG ATG GCC ACA TAC TTA TTG GAA GAG AAT  
 ser met ala thr tyr leu leu glu glu asn  
 2971/991  
 CCT GAG GCG TAT CAC CAC GTC TTA CAT TCT  
 pro glu ala tyr his his val leu his ser  
 3031/1011  
 ATT GCG TAT GCA GAG ATT CCT GAT GAG TCC  
 ile arg tyr ala glu ile pro asp glu ser  
 3091/1031  
 TGC TGC TTG ACA CTG ATG GAC AGA  
 leu lys arg cys leu thr leu met asp arg  
 3151/1051  
 TCA GGA TTT AGC CCT AAG GAT CCT AAG  
 ala tca gga ttt agc cct aag gat cct aag  
 3211/1071  
 CAA ACA ATC TGC AAT CAT GAA CAT TAC ATT  
 thr thr ile cys asn his glu his tyr ile

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3241/1081	3271/1091
CCT CTG AAC TTG CCA ATG GCA TTT GCA AAG	CCT AAA TTA CAG AGA GTT CAA GAT TCC AAT
pro leu asn leu pro met ala phe ala lys	pro lys leu gln arg val gln asp ser asn
3301/1101	3331/1111
CTT GAA TAC AGT TTA TCA GAT GAG TAT TGC	AAG CAT CAC TTC TTG GTT GGC CTA CTT CTG
leu glu tyr ser leu ser asp glu tyr cys	lys his his phe leu val gly leu leu leu
3361/1121	3391/1131
CGG GAA ACC TCC ATT GCT CTT CAA GAC AAC	TAT GAG ATC AGA TAC ACA GCT ATC TCA GTC
arg glu thr ser ile ala leu gln asp asn	tyr glu ile arg tyr thr ala ile ser val
3421/1141	3451/1151
ATA AAG AAT CTT TTG ATA AAA CAT GCA TTT	GAT ACT AGA TAC CAG CAC AAG AAC CAG CAA
ile lys asn leu leu ile lys his ala phe	asp thr arg tyr gln his lys asn gln gln
3481/1161	3511/1171
GCC AAA ATA GCG CAG TTG TAC CTC CCA TTT	GTC GGA CTG CTC TTG GAA AAT ATC CAG CGA
ala lys ile ala gln leu tyr leu pro phe	val gly leu leu leu glu asn ile gln arg
3541/1181	3571/1191
CTG GCA GGC GCA GAT ACT CTG TAT TCC TGT	GCA GCC ATG CCT AGT TCT GCA TCT AGG GAT
leu ala gly arg asp thr leu tyr ser cys	ala ala met pro ser ser ala ser arg asp
3601/1201	3631/1211
GAG TTT CCA TGT GGC TTT GTT TCA CCT ACA	AAC AGA GGG AGC CTG GCC AGT GAC AAA GAC
glu phe pro cys gly phe val ser pro thr	asn arg gly ser leu ala ser asp lys asp
3661/1221	3691/1231
ACA GCC TAT GGG TCA TTT CAA AAT GGT CAT	GGA ATT AAG AGG GAA GAT TCA AGA GGT TCC
thr ala tyr gln ser phe gln asn gly his	gly ile lys arg gly asp ser arg gly ser
3721/1241	3751/1251
CTT ATT CCT GAA GGA GCA ACA GGA TTT CCA	GAC CCT GGG AGC ACT AGT GAA AAC ACA CGA
leu ile pro glu gly ala thr gly phe pro	asp pro gly ser thr ser glu asn thr arg
3781/1261	3811/1271
CAG AGT TCT TCA AGG AGT AGT GTA TCC CAG	TAT AAT GGT CTG GAT CAG TAT GAA ATC AGA
gln ser ser ser arg ser ser val ser gln	tyr asn arg leu asp gln tyr glu ile arg
3841/1281	3871/1291
AAC CTC TTG ATG TGC TAC TTA TAC ATA GTA	AAG ATG ATT TCT GAA GAT ACT CTC TTG ACT
asn leu leu met cys tyr leu tyr ile val	lys met ile ser glu asp thr leu leu thr
3901/1301	3931/1311
TAC TGG AAT AAA GTG TCT CCT CAG GAG CTC	ATA AAC ATT CTT GTA CTT CTA GAA GTA TGT
tyr trp asn lys val ser pro gln glu leu	ile asn ile leu val leu leu glu val cys
3961/1321	3991/1331
TTG TTT CAC TTC CGA TAT ATG GGG AAA AGA	AAC ATA GCA AGG GTA CAT GAT GCC TGG CTA
leu phe his phe arg tyr met gly lys arg	asn ile ala arg val his asp ala trp leu
4021/1341	4051/1351
TCC AAA CAC TTT GGA ATA GAT AGA AAA TCA	CAA ACT ATG CCA GCT CTT CGA AAC AGA TCA
ser lys his thr thr gly ile asp arg lys ser	gln thr met pro ala leu leu glu arg ser
4081/1361	4111/1371
GGG GTG ATG CAA GCT CGG CTT CAA CAT CTC	AGC AGC TTA GAA AGC TCA TTC ACA CTT AAT
gly val met gln ala arg leu gln his leu	ser ser leu glu ser ser phe thr leu asn
4141/1381	4171/1391
CAC AGT TCT GCA ACA ACG GAA GCA GAC ATT	TTC CAC CAG GCG CTT CTG GAA GGC AAT ACT
his ser ser ala thr thr thr glu ala asp ile	phe his gln ala leu leu glu gly asn thr
4201/1401	4231/1411
GCT ACT GAA GTA TCT CTG ACA GTA CTA GAG	ACG ATC TCC TTT TTT ACC CAG TGC TTC AAG
ala thr glu val ser leu thr val leu glu	thr ile ser phe phe thr gln cys phe lys
4261/1421	4291/1431
AAC CAA CTT TTA AAT AAT GAT GGT CAC AAC	CCA CTA ATG AAA AAA GTA TTT GAT ATT CAC
asn gln leu leu asn asn asp gly his asn	pro leu met lys lys val phe asp ile his
4321/1441	4351/1451
CTT GCT TTT CTT AAA AAT GGA CAA TCT GAA	GTG TCA CTG AAG CAT GTC TTT GCC TCA CTG
leu ala phe leu lys asn gly gln ser glu	val ser leu lys his val phe ala ser leu

4381/1461  
 AGA TCT TTC ATC AGT AAG TTT CCC TCA GCC  
 arg ser phe ile ser lys phe pro ser ala phe phe lys gly arg val asn met cys ala  
 4441/1481  
 GCA TTT TGC TAT GAG GTT TTA AAG TGC TGT ACT TCA AAG ATT AGC TCA ACC AGG AAT GAG  
 ala phe cys tyr glu val leu lys cys cys thr ser lys ile ser ser thr arg asn glu  
 4501/1501  
 GCA TCT GCA CTT TTG TAT CTT TTG ATG AGA AAC AAC TTT GAA TAT ACC AAG AGG AAA ACC  
 ala ser ala leu leu tyr leu leu met arg asn asn phe glu tyr thr lys arg lys thr  
 4561/1521  
 TTT CTG AGG ACA CAC TTG CAG ATA ATC ATT GCT GTG AGT CAG CTA ATA GCT GAT GTA GCA  
 phe leu arg thr his leu gln ile ile ile ala val ser gln leu ile ala asp val ala  
 4621/1541  
 CTA AGT GGA GGA TCG AGA TTT CAA GAG TCT TTA TTC ATT ATC AAT AAC TTT GCA AAT AGC  
 leu ser gly gly ser arg phe gln glu ser leu phe ile ile asn asn phe ala asn ser  
 4681/1561  
 GAC AGA CCT ATG AAG GCA ACT GCT TTT CCC ACA GAA GTC AAA GAT TTG ACC AAG AGG ATC  
 asp arg pro met lys ala thr ala phe pro thr glu val lys asp leu thr lys arg ile  
 4741/1581  
 CGC ACC GTT CTT ATG GCC ACT GCC CAA ATG AAG GAA CAT GAG AAA GAC CCT GAA ATG CTA  
 arg thr val leu met ala thr ala gln met lys glu his glu lys asp pro glu met leu  
 4801/1601  
 ATT GAT CTC CAG TAT AGC TTA GCT AAA TCT TAT GCC AGC ACA CCA GAG CTG AGG AAA ACT  
 ile asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr  
 4861/1621  
 TGG CTT GAC AGC ATG GCC AAA ATT CAT ATA AAA AAT GGA GAT TTT TCT GAG GCT GCA ATG  
 trp leu asp ser met ala lys ile his ile lys asn gly asp phe ser glu ala ala met  
 4921/1641  
 TGT TAT GTC CAT GTA GCG GCT CTA GTT GCA GAA TTT CTT CAC CGA AAG AAA TTA TTC CCT  
 cys tyr val his val ala ala leu val ala glu phe leu his arg lys lys leu phe pro  
 4981/1661  
 AGT GGG TGT TCA GCG TTC AAG AAA ATT ACT CCC AAT ATA GAT GAA GAA GGA GCC ATG AAA  
 ser gly cys ser ala phe lys lys ile thr pro asn ile asp glu glu gly ala met lys  
 5041/1681  
 GAA GAT GCG GCG ATG ATG GAT GTT CAT TAC AGT GAA GAG GTT TTG CTG GAA TTG CTA GAA  
 glu asp ala gly met met asp val his tyr ser glu glu val leu leu glu leu leu glu  
 5101/1701  
 CAG TGT GTG GAT GGT TTG TGG AAG GCA GAG CGA TAT GAA GTA ATT TCT GAG ATT TCC AAG  
 gln cys val asp gly leu trp lys ala glu arg tyr glu val ile ser glu ile ser lys  
 5161/1721  
 TTG ATT ATT CCA ATT TAT GAG AAA CGC CGT GAA TTT GAG AAA CTG ACT CAA GTT TAT AGA  
 leu ile ile pro ile tyr glu lys arg arg glu phe glu lys leu thr gln val tyr arg  
 5221/1741  
 ACT CTC CAT GGC GCT TAC ACA AAA ATT TTG GAG GTT ATG CAC ACC AAA AAA CGA CTT TTA  
 thr leu his gly ala tyr thr lys ile leu glu val met his thr lys lys arg leu leu  
 5281/1761  
 GGT ACT TTC TTT AGA GTT GGC TTT TAT GGC CAG TCT TTT TTT GAA GAA GAA GAT GGA AAG  
 gly thr phe phe arg val ala phe tyr gly gln ser phe phe glu glu glu asp gly lys  
 5341/1781  
 GAG TAT ATC TAT AAG GAA CCC AAG CTC ACT GGC CTT TCA GAG ATT TCC TTG AGA CTT GTG  
 glu tyr ile tyr lys glu pro lys leu thr gly leu ser glu ile ser leu arg leu val  
 5401/1801  
 AAA CTT TAC GGG GAG AAA TTT GGT ACT GAA AAT GTC AAA ATA ATT CAG GAT TCA GAC AAG  
 lys leu tyr gly glu lys phe gly thr glu asn val lys ile ile gln asp ser asp lys  
 5461/1821  
 GTA AAT GCC AAA GAG CTT GAT CCA AAA TTC GCT CAT ATA CAA GTC ACT TAT GTG AAG CCG  
 val asn ala lys glu leu asp pro lys phe ala his ile gln val thr tyr val lys pro

24/95

5521/1841	5551/1851
TAT TTT GAT GAC AAA GAA CTC ACA GAA AGA	AAG ACG GAG TTT GAA AGA AAT CAT AAT ATC
tyr phe asp asp lys glu leu thr glu arg	lys thr glu phe glu arg asn his asn ile
5581/1861	5611/1871
AAC AGA TTT GTT TTT GAG GCC CCA TAT ACA	TTA TCA GGC AAG AAA CAA GGT TGC ATT GAA
asn arg phe val phe glu ala pro tyr thr	leu ser gly lys lys gln gly cys ile glu
5641/1881	5671/1891
GAA CAG TGC AAG CGT CGT ACT ATC TTG ACC	ACT TCA AAC TCA TTT CCA TAT GTA AAA AAG
glu gln cys lys arg arg thr ile leu thr	thr ser asn ser phe pro tyr val lys lys
5701/1901	5731/1911
AGG ATA CCT ATA AAC TGT GAA CAG CAG GTG	AAT TTA AAA CCA ATT GAT GTT GCT ACT GAT
arg ile pro ile asn cys glu gln gln val	asn leu lys pro ile asp val ala thr asp
5761/1921	5791/1931
GAA ATC AAA GAT AAA ACT GCA GAG CTA CAC	AAG CTC TGC TCC TCT GTT GAC GTG GAC ATG
glu ile lys asp lys thr ala glu leu his	lys leu cys ser ser val asp val asp met
5821/1941	5851/1951
ATT CAG CTT CAG CTA AAG TTG CAG GGC TGT	GTC TCT GTG CAG GTC AAT GCT GGT CCA TTA
ile gln leu gln leu lys leu gln gly cys	val ser val gln val asn ala gly pro leu
5881/1961	5911/1971
GCA TAT GCG AGG GCT TTC TTA AAT GAA AGT	CAA GCT AAC AAG TAT CCA CCT AAA AAA GTG
ala tyr ala arg ala phe leu asn glu ser	gln ala asn lys tyr pro pro lys lys val
5941/1981	5971/1991
AAT GAG TTG AAG GAC ATG TTT AGA AAA TTC	ATA CAA GCA TGC AGC ATT GCA CTT GAA CTA
asn glu leu lys asp met phe arg lys phe	ile gln ala cys ser ile ala leu glu leu
6001/2001	6031/2011
AAT GAG CGG CTA ATT AAA GAG GAT CAA ATT	GAG TAC CAT GAA GGG CTA AAG TCA AAT TTC
asn glu arg leu ile lys glu asp gln ile	glu tyr his glu gly leu lys ser asn phe
6061/2021	6091/2031
AGA GAC ATG GTA AAA GAA CTG TCT GAC ATT	ATC CAT GAG CAG ATA CTA CAA GAA GAC ACA
arg asp met val lys glu leu ser asp ile	ile his glu gln ile leu gln glu asp thr
6121/2041	6151/2051
ATG CAT TCT CCC TGG ATG AAC AAC ACA TTA	CAT GTA TTT TGT GCA ATT AGT GGT ACA TCA
met his ser pro trp met asn asn thr leu	his val phe cys ala ile ser gly thr ser
6181/2061	6211/2071
AGT AAC AGA GGT TAT GGT TCC CCA AGA TAC	GCG GAA GTA TGA AGA GAT TTG GAA GGA AAT
ser asn arg gly tyr gly ser pro arg tyr	ala glu val OPA
6241/2081	6271/2091
GGC AAT GAG GAC ACT CTT TCT CAG GAA TAT	TTG GAG CTG TGC AAC TGT TAG CAT TTA GAG
6301/2101	6331/2111
ATT TGA TAT GTG TGG AGT GTT GCC TCC TGA	CAC CAA AAT CGT CAT GCT TTC ATA CAG GGT
6361/2121	6391/2131
GCT TGT ATC TGT AAA TAT TTA AGC AAC TCG	AAG TGC CTG AAA AAT TGC AGC ACT GTG CTT
6421/2141	6451/2151
GCT TGT ACT TTT TTT AGG TAA ATC TAT ATG	CTG AAA AGT AGA GCT CAA AAC CAT TCG TTC
6481/2161	6511/2171
AAT TGC TTA GTT ACC ACT TAC TAA TAA TGA	GAA TAT GTA AAA TGT ATA AAT GGA AAC CCA
6541/2181	6571/2191
AAT AAA AGG TAA CAA ACT TAT TTG TAA AAA	AAA AAA AAA



## E. Mouse CLASP-5 cDNA sequence

-282/1  
 GGA CAC TGA CAT GGA CTG AAG GAG TAG AAA ACT TCC TCA TAC AAG CAC AAG CCA CAG CCA  
 -252/11  
 -222/21  
 CTC TCT CTG GCT GAT CTA GTG GTT ATC TTG AGA AGG TTA GGT TCT TTT TTG TTT CTA CTT  
 -192/31  
 -162/41  
 ATT ACT TCA AAG CCA CTT CTG CTC TTC GAA ATT TTG TAA CCT TCC CCT GTT TCC TGT AGC  
 -132/51  
 -102/61  
 CGC CAT TTT GTC GCC CGT GAC AGT TTA CCC ACC GCG TTA ACT GTG TGT CTT CAG CCT CAG  
 -72/71  
 -42/81  
 CTT TAT GAG CCT GCT GAG CCA GTG GAC TTT GAA GGA CTC GTG ATG ACA CAC TTA AAC AGC  
 met thr his leu asn ser  
 19/101  
 TTG GAT GCA GAG CTG GCC CAG GAG CTG GGG GAC CTC ACC GAT GAC GAC CTG CAT GTG GCC  
 leu asp ala glu leu ala gln glu leu gly asp leu thr asp asp asp leu his val ala  
 49/111  
 79/121  
 TTC ACA CCC AAA GAA TGT AGG ACT TTG CAG CAC TCT CTG CCA GAG GAA GGA GTT GAA CTG  
 phe thr pro lys glu cys arg thr leu gln his ser leu pro glu glu gly val glu leu  
 109/131  
 139/141  
 GAT CCT CAC GTC AGA GAC TGT GTT CAG ACC TAT ATT CGA GAG TGG CTG ATT GTA AAC CGG  
 asp pro his val arg asp cys val gln thr tyr ile arg glu trp leu ile val asn arg  
 169/151  
 199/161  
 AAA AAC CAA GGA AGT TCA GAG TTT TGC AGC TTT AAA AAG ACG GGA TCT CGC AGA GAT TTT  
 lys asn gln gly ser ser glu phe cys ser phe lys lys thr gly ser arg arg asp phe  
 289/191  
 259/181  
 CAG AAG ACG CTT CAG AAA CAG ACG TTT GAG TCA GAA ACC TTG GAG TGC AGT GAA CCG GAC  
 gln lys thr leu gln lys gln thr phe glu thr leu glu cys ser glu pro asp  
 349/211  
 319/201  
 ACT CAG ACA GGA CCC CGT CAT CCC TTA AAC GTG CTG TGT GAC GTG TCT GGG AAG GGC CCC  
 thr gln thr gly pro arg his pro leu asn val leu cys asp val ser gly lys gly pro  
 409/231  
 379/221  
 CTC ACT TCT TGT GAC TTC GAC CTC CGC AGC CTG CAG CCT GAT GAG CGG CTG GAA AAC CTG  
 leu thr ser cys asp phe asp leu arg ser leu gln pro asp glu arg leu glu asn leu  
 469/251  
 439/241  
 CTC CAG CTT GTG AGC GCT GAG GAC TTT GAG AAG GAG AAG GAG GCC CGC AAG ACC AAT  
 leu gln leu val ser ala glu asp phe glu lys glu lys glu ala arg lys thr asn  
 529/271  
 499/261  
 CGG CCG GCT GAG CTC TTT GCC CTC TAT CCG CCC GTG GAT GAG GAG GAT GCT GTG GAA ATA  
 arg pro ala glu leu phe ala leu tyr pro pro val asp glu glu asp ala val glu ile  
 589/291  
 559/281  
 CGT CCA GTA CCT GAA TGT CCT AAG GAA CAT CTG GGC AAC AGA ATA TTG GTC AAG GTG CTG  
 arg pro val pro glu cys pro lys glu his leu gly asn arg ile leu val lys val leu  
 649/311  
 619/301  
 ACT CTG AAG TTT GAG ATT GAA ATT GAA CCT CTG TTT GCC AGT ATT GCC CTC TAT GAC GTT  
 thr leu lys phe glu ile glu ile glu pro leu phe ala ser ile ala leu tyr asp val  
 709/331  
 679/321  
 AAA GAA AGG AAA AAG ATC TCA GAA AAT TTC CAC TGT GAC CTG AAC TCC GAC CAG TTC AAA  
 lys glu arg lys lys ile ser glu asn phe his cys asp leu asn ser asp gln phe lys  
 769/351  
 739/341  
 GGG TTT CTG CGA GCT CAC ACA CCC TCG ATT GAC CCA TCG AGT CAG GCT AGG TCT GCC GTG  
 gly phe leu arg ala his thr pro ser ile asp pro ser ser gln ala arg ser ala val

799/361  
 TTC TCC GTC ACC TAC CCA TCT TCA GAC ATC 829/371  
 phe ser val thr tyr pro ser ser asp ile tyr leu val val lys ile glu lys val leu  
 859/381  
 CAG CAA GAA GAG ATT GCA GAC TGT GCA GAA 889/391  
 gln gln gln gly glu ile ala asp cys ala glu pro tyr met ile ile lys glu ser asp gly  
 919/401  
 GGA AAG AGT AAA GAA AAG GTT GAA AAA CTA AAA CTT CAA GCT GAA TCC TTC TGC CAA CGT  
 gly lys ser lys glu lys val glu lys leu lys leu gln ala glu ser phe cys gln arg  
 979/421  
 TTT GGG AAA TAC CGG ATG CCC TTC GCC TGG GCC CCC ATT AGC TTA GCA AGC TTC TTC AAC  
 leu gly lys tyr arg met pro phe ala trp ala pro ile ser leu ala ser phe phe asn  
 1039/441  
 GTC TCC ACC CIT GAA AGG GAG AGC ACA GAT GTG GAG CCT GGG GTT GGG AGG AAC TCT GTG  
 val ser thr leu glu arg glu ser thr asp val glu pro gly val gly arg asn ser val  
 1099/461  
 GGT GAG AAG AGG AGC TTG TCC CAA TCC AGG AGG CCC TCT GAG CGA ACC CTC TCC TTG GAG  
 gly glu lys arg ser leu ser gln ser arg arg pro ser glu arg thr leu ser leu glu  
 1159/481  
 GAA AAT GAA GTT GGA TCC AAC TTC AAA GCC ACC ACC TTG GCC ACC AAC ATC TTC TTC AAA  
 glu asn gly val gly ser ser asn phe lys ala thr thr leu ala thr asn ile phe phe lys  
 1219/501  
 CAG GAG GGA GAT CGC CTT AGT GAT GAA GAC TTG TTC AAG TTT TTA GCT GAC TAC AAG AGA  
 gln glu gly asp arg leu ser asp glu asp leu phe lys phe leu ala asp tyr lys arg  
 1279/521  
 TCT TCA TCC CTA CAG CGA AGA GTC AAA TCC ATC CCG GGC TCA CTG AGG CTG GAG ATA TCC  
 ser ser ser leu gln arg arg val lys ser ile pro gly ser leu arg leu glu ile ser  
 1339/541  
 CCA GCT CCC GAC GTG ATG AAC TGC TGC CTG ACG CCC GAG ATG CTG CCA GTC AAA CCT TTT  
 pro ala pro asp val met asn cys cys leu thr pro glu met leu pro val lys pro phe  
 1399/561  
 CCT GAA AAT CGG ACG CGT CCA CAC AAG GAG ATT TTG GAA TTT CCG ATC CGG GAG GTG TAC  
 pro glu asn arg thr arg pro his lys glu ile leu glu phe pro ile arg glu val tyr  
 1459/581  
 GTC CTT CAC ACT GTG TAC AGA AAC CTT CTG TAC GTA TAC CCC CAG CGA CTG AAC TTC GCT  
 val pro his thr val tyr arg asn leu leu tyr val tyr pro gln arg leu asn phe ala  
 1519/601  
 AGC AAG CTA GCA TCT GCC CGG AAC ATC ACA ATA AAG ATT CAG TTT ATG TGC GGA GAA GAC  
 ser lys leu ala ser ala arg asn ile thr ile lys ile gln phe met cys gly glu asp  
 1579/621  
 CCC AGC AAT GCT ATG CCG GTC ATC TTT GGC AAG TCC AGT GGG CCT GAA TTT CTG CAG GAA  
 pro ser asn ala met pro val ile phe gly lys ser ser gly pro glu phe leu gln glu  
 1639/641  
 GTA TAT ACA GCT ATT ACA TAC CAT AAT AAG TCT OCT GAC TTT TAC GAA GAA GTG AAA ATT  
 val tyr thr ala ile thr tyr his asn lys ser pro asp phe tyr glu glu val lys ile  
 1699/661  
 AAG CTC CCT GCC AAG CTC ACA GTG AAT CAT CAC CTC CTC TTC ACC TTC TAC CAC ATC AGC  
 lys leu pro ala lys leu thr val asn his his leu leu phe thr phe tyr his ile ser  
 1759/681  
 TGT CAG CAG AAG CAA GGG GCC TCC GGA GAA AGC CTT CTG GGG TAC TCG TGG CTG CCG ATT  
 cys gln gln lys gln gly ala ser gly glu ser leu leu gly tyr ser tgp leu pro ile  
 1819/701  
 CTG TTA AAG GAA CGT CTT CAA ACC GGA TCC TAC TGT CTG CCT GTT GCC TTG GAA AAA CTA  
 leu leu asn glu arg leu gln thr gly ser tyr cys leu pro val ala leu glu lys leu  
 1879/721  
 CCA CCC AAC TAC TCC ATA CAT TCT GCT GAG AAA GTC CCT TTA CAG AAT CCT CCC ATT AAG  
 pro pro asn tyr ser ile his ser ala glu lys val pro leu gln asn pro pro ile lys

27/95

<p>1939/741  TGG GTC GAG GGC CAT AAG GGA GTA TTT AAT  trp val glu gly his lys gly val phe asn  1999/761  ACC CAG GAT AAC CAC CTG GAG AAG TTC TTC  thr gln asp asn his leu glu lys phe phe  2059/781  AGC TTC CCT ATC CGT GTG CTG GAC CAG AAG  ser phe pro ile arg val leu asp gln lys  2119/801  AAA CTC AGC ATC ATC TGC CTC AAC TCC TCC  lys leu ser ile ile cys leu asn ser ser  2179/821  CTG GTG CTC GAC AAG CTG TTC CAG CTT TCC  leu val leu asp lys leu phe gln leu ser  2239/841  GCA AAC TTC TCC CAG TTT GCC TTC GAG TCT  ala asn phe ser gln phe ala phe glu ser  2299/861  AGC AAG GAC CTG AGG AAG GAC CAG CAC GGA  ser lys asp leu arg lys asp gln his gly  2359/881  TAC GTG TTC CGG CTG CCG GAA CTG CAC AGG  tyr val phe arg leu pro glu leu his arg  2419/901  GTA GTC CCC GAC CCC CGA TAC CAC ACA TAT  val val pro asp pro arg tyr his thr tyr  2479/921  AAG CTG ATG CAG GCC CGT GTG ATG AGC AGC  lys leu met gln ala arg val met ser ser  2539/941  GCA GCC GAT GAG GAA GTT AAG AAC ATC ATG  ala ala asp glu glu val lys asn ile met  2599/961  CGG ATG TCT TAC TAT TGC TCT GGC AAT AGT  arg met ser tyr tyr cys ser gly asn ser  2659/981  CCA GTC AGC AAA AAG CAT TTC CAT GAG GAG  pro val ser lys lys his phe his glu glu  2719/1001  GTA GTG AGA GAA AGC GTC TTC AAG TAC GCC  val val arg glu thr val phe lys tyr ala  2779/1021  ATG GCG CAG TAT GTC CAT AAC CTG GAT AAA  met ala gln tyr val his asn leu asp lys  2839/1041  GAC CGC TTC AAA GAT GAC ATA ACT ACC ATT  asp-arg phe lys asp asp ile thr thr ile  2899/1061  CTT TTA GTG AAA CCT CAG AAG GAA AGC GAG  leu leu val lys pro gln lys glu ser glu  2959/1081  TTC TTC CTG TAT GAC CTC CTG TCA ATC ATG  phe phe leu tyr asp leu leu ser ile met  3019/1101  CAT TAC TGC AGC CAG CTG TCA GCC AAG CTG  his tyr cys ser gln leu ser ala lys leu</p>	<p>1969/751  ATT GAA GTG CAA GCT GTT TCT TCC GTC CAC  ile glu val gln ala val ser ser val his  2029/771  ACC CTT TGC CAC TCC CTG GAG AGC CAG GTG  thr leu cys his ser leu glu ser gln val  2089/791  ATC ACC GAG AGC ACG CTG GAG CAC GAG CTG  ile thr glu ser thr leu glu his glu leu  2149/811  CGC CTG GAG CCC CTC GTG CTC TTC CTC CAC  arg leu glu pro leu val leu phe leu his  2209/831  GTG CAG CCC ATG GTC ATT GCT GGC CAA ACA  val gln pro met val ile ala gly gln thr  2269/851  GTG GTG GCC ATT GCC AAT AGC CTG CAC AAC  val val ala ile ala asn ser leu his asn  2329/871  AGG AAC TGC CTT CTG GCC TCC TAT GTG CAC  arg asn cys leu leu ala ser tyr val his  2389/891  GAT ACA TCC AAG TCA GGT GGC CCC ATC ACC  asp thr ser lys ser gly gly pro ile thr  2449/911  GGA CGC ACA TCT GCC GCT GCA GTG AGT TCA  gly arg thr ser ala ala ala val ser ser  2509/931  AGC AAC CCA GAC CTG ACT GGG TCA CAC TGT  ser asn pro asp leu thr gly ser his cys  2569/951  TCT TCA AAG ATT GCC GAT CGC AAC TGC AGC  ser ser lys ile ala asp arg asn cys ser  2629/971  GAT GCG CCA GGT TCA ACT GCA GCC CCA AGA  asp ala pro gly ser thr ala ala pro arg  2689/991  CTT GCC CTG CAG ATG GTG GTC AGC ACT GGA  leu ala leu gln met val val ser thr gly  2749/1011  TGG TTC TTC TTT GAG CTT CTG GTG AAA AGC  trp phe phe glu leu leu val lys ser  2809/1031  CGG GAC AGT TTT CGG AGG ACT CGT TTT TCT  arg asp ser phe arg arg thr arg phe ser  2869/1051  GTT AAT GTG GTC ACC TCG GAG ATA GCA GCC  val asn val val thr ser glu ile ala ala  2929/1071  CAG GCA GAA AAG ATC AAC ATC AGC CTT GCC  gln ala glu lys ile asn ile ser leu ala  2989/1091  GAC AGA GGC TTC GTG TTC AAC CTC ATC AAG  asp arg gly phe val phe asn leu ile lys  3049/1111  AAT ATC CTT CCA ACG CTC ATC TCC ATG CGG  thr leu ile ser met arg</p>
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3079/1121 CTG GAA TTC CTG AGG ATC CTC TGC AGC CAT GAG CAC TAC CTC AAC TTG AAC CTC CTC TTC  
 leu glu phe leu arg ile leu cys ser his glu his tyr leu asn leu asn leu leu phe  
 3139/1141  
 ATG AAT ACC GAC ACC GCA CCA GCA TCT CCC TGC CCC TCC ATA TCC TCC CAG AAC TCG AGT  
 met asn thr asp thr ala pro ala ser pro cys pro ser ile ser ser gln asn ser ser  
 3199/1161  
 TCC TGC TCC AGT TTC CAG GAC CAA AAG ATT GCC AGC ATG TTC GAT CTG ACC CCG GAG TAC  
 ser cys ser ser phe gln asp gln lys ile ala ser met phe asp leu thr pro glu tyr  
 3259/1181  
 CGG CAG CAC CAC TTC CTT ACA GGG CTG CTC TTC ACG GAG CTG GCT GTT GCC CTG GAT GCT  
 arg gln gln his phe leu thr gly leu leu phe thr glu leu ala val ala leu asp ala  
 3319/1201  
 GAG GGG GAT GGA ATT AGC AGA GTA CAG AAG AAA GCC CTG AGT GCC ATC CAC AGC CTT CTG  
 glu gly asp gly ile ser arg val gln arg lys ala val ser ala ile his ser leu leu  
 3379/1221  
 TGT TCT CAC GAC CTG GAT CCA CGG TGT CGC AAA CCG GAA GTG AAA GTC AAA ATC GCC GCC  
 cys ser his asp leu asp pro arg cys arg lys pro glu val lys val lys ile ala ala  
 3439/1241  
 CTT TAC CTG CCG TTG GTC GGC ATC ATT CTG GAC GCT CTG CCA CAG CTC TAT GAC TTT ACA  
 leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu tyr asp phe thr  
 3499/1261  
 GAT GCT CGC AGT GGA AGG AGT CGT GCC AGT GGC TCG TAT GAA GAA CAA GAT GTG GCC AAC  
 asp ala arg ser gly arg ser arg ala ser gly ser tyr glu glu gln asp val ala asn  
 3559/1281  
 GGA ATC AAC CAG AAT GTG GCC CTG GCC ATA GCG GGG AAT CAC TTT AAT TTG AAG ACC AGT  
 gly ile asn gln asn val ala leu ala ile ala gly asn his phe asn leu lys thr ser  
 3619/1301  
 GGA GCA ATG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAT GCA GAC ACC ACC  
 gly ala met leu ser ser leu pro tyr lys gln tyr asn met leu asn ala asp thr thr  
 3679/1321  
 CGC CAC CTC ATG ATT TGC TTC CTG TGG ATC ATG AAA AAT GCT GAT CAG AGC CTC ATC AGG  
 arg his leu met ile cys phe leu trp ile met lys asn ala asp gln ser leu ile arg  
 3739/1341  
 AAG TGG ATC GCT GAC CTG CCT TCC ATG CAG CTC AAT AGG ATT CTG GAC CTG CTG TTC ATC  
 lys trp ile ala asp leu pro ser met gln leu asn arg ile leu asp leu leu phe ile  
 3799/1361  
 TGT GTC TCC TGC TTT GAA TAC AAG GGA AAG CAG AGT TCT GAC AAA GTC AGT AAC CAG GTC  
 cys val ser cys phe glu tyr lys gly lys gln ser ser asp lys val ser asn gln val  
 3859/1381  
 CTG CAG AAG TCA AGA GAC GTG AAC GCC AAG CTG GAA GAG GCC CTG CTC CGT GGG GAA GGA  
 leu gln lys ser arg asp val lys ala lys leu glu glu ala leu leu arg gly glu gly  
 3919/1401  
 GCC CGT GGG GAG ATG ATG CGC CGT CGC ATT CCA GGG ACT GAC CGG TTT CCA GGC ATA AAT  
 ala arg gly glu met met arg arg arg ile pro gly thr asp arg phe pro gly ile asn  
 3979/1421  
 GAA AAT CTG AGA TGG AGG AAA GAG CAG ACA CAG TGG CGG CAG GCT AAT GAG AAG CTG GAC  
 glu asn leu arg trp arg lys glu gln thr gln trp arg gln ala asn glu lys leu asp  
 4039/1441  
 AAA ACA AAG GCA GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAC CTG GCT ACA GAA GCT  
 lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala thr glu ala  
 4099/1461  
 AAT TTG ATC ATC CTG GAT ATG CAG GAG AAC ATC ATC CAG GCA AGC TCC GCC CTG GAC TGT  
 asn leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala leu asp cys  
 4159/1481  
 AAA GAC AGC CTG CTG GGA GGT GTC CTC CGG GTC CTG GTG AAT TCT CTG AGC TGT GAC CAG  
 lys asp ser leu leu gly gly val leu arg val leu val asn ser leu ser cys asp gln

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4219/1501  
AGC ACC ACC TAC CTG ACT CAC TGT TTC GCA  
ser thr thr tyr leu thr his cys phe ala  
4279/1521  
GAC CTG CTG TTC GAG GAG GAG ATG GAG CAG  
asp leu leu phe glu glu glu met glu gln  
4339/1541  
CAC TGC AGC AGC AGC ATG GAC GTC ACA CGG  
his cys ser ser ser met asp val thr arg  
4399/1561  
ATG CGG TTC AGC TTC GGA GCC ACC AGT AAC  
met arg phe ser phe gly ala thr ser asn  
4459/1581  
GCA CTG GCA TCC CTG GTA GGC AAA GCA CCA  
ala leu ala ser leu val gly lys ala pro  
4519/1601  
TTA AGG ACA ATT TTG GCC TAT TCA GAA GAG  
leu arg thr ile leu ala tyr ser glu glu  
4549/1621  
ATG CAG GTG GAG GAA CTT CTC TGC AAT CTG  
met gln val glu glu leu leu cys asn leu  
4639/1641  
AGG GAA TTC CAG GAA GAC CCT GAG ATG CTT  
arg glu phe gln glu asp pro glu met leu  
4699/1661  
TAC CAG GCA TCG CCT GAC CTG CGG CTG ACT  
tyr gln ala ser pro asp leu arg leu thr  
4759/1681  
AAG AAG AAG TGC TTC ACA GAG GCC GCC ATG  
lys lys lys cys phe thr glu ala ala met  
4819/1701  
GAG TAC CTG AGC ATG CTG GAG GAC CAC AGC  
glu tyr leu ser met leu glu asp his ser  
4879/1721  
AAT ATT TCT TCC AAT GTG CTT GAG GAG TCT  
asn ile ser ser ser asn val leu glu glu ser  
4939/1741  
GAG GAC GGC GTA TGC TCT GGT CGG TAC TTC  
glu asp gly val cys ser gly arg tyr phe  
4999/1761  
CAG GCT CGG GAG CTC TTC AGC ACG GGA GGC  
gln ala ala glu leu phe ser thr gly gly  
5059/1781  
CTG GTC ATC CCT ATC CTG GAG GCA CAC AGA  
leu val ile pro ile leu glu ala his arg  
5119/1801  
AAG CTG CAG AAG GCC TTC GAT AAC ATC ATC  
lys leu gln lys ala phe asp asn ile ile  
5179/1821  
TAC TTC CGA GTT GGT TTC TAC GGA TCC CGA  
tyr phe arg val gly phe tyr gly ser arg  
5239/1841  
TAC AAG GAA CCC GCA ATC ACG AAG CTC CCG  
tyr lys glu pro ala ile thr lys leu pro  
5299/1861  
GGC CAG TGT TGT GGT GCA GAG TTT GTG GAA  
gly gln cys phe gly ala glu phe val glu  
4249/1511  
ACC CTC CGA GCC CTC ATC GCC AAG TTT GGA  
thr leu arg ala leu ile ala lys phe gly  
4309/1531  
TGT GCT GAC CTG TGT CAG CGG GTG CTA CAT  
cys ala asp leu cys gln arg val leu his  
4369/1551  
AGC CAA GCC TGC GCC ACC CTC TAC CTC CTC  
ser gln ala cys ala thr leu tyr leu leu  
4429/1571  
TTT GCA AGG GTA AAG ATG CAA GTG ACC ATG  
phe ala arg val lys met gln val thr met  
4489/1591  
asp phe asn glu glu his leu arg arg ser  
4549/1611  
GAC TTC AAC GAA GAG CAC CTG AGA AGG TCC  
asp phe asn glu glu his leu arg arg ser  
4609/1631  
AAC AGC ATT CTG TAC GAC ACA GTG AAG ATG  
asn ser ile leu tyr asp thr val lys met  
4669/1651  
ATG GAC CTC ATG TAC AGA ATT GCC AAG AGC  
met asp leu met tyr arg ile ala lys ser  
4729/1671  
TGG CTC CAG AAC ATG GCA GAG AAA CAC ACT  
trp leu gln asn met ala glu lys his thr  
4789/1691  
TGC CTG GTG CAT GCA GCC GCC CTG GTG GCC  
cys leu val his ala ala ala leu val ala  
4849/1711  
TAC CTG CCG GTG GGC AGC GTC AGC TTT CAG  
tyr leu pro val gly ser val ser phe gln  
4909/1731  
GCA GTC TCT GAT GAC ACC TTG TCA CCT GAT  
ala val ser asp asp thr leu ser pro asp  
4969/1751  
ACT GAG AGT GGC CTG GTG GGC CTC CTG GAG  
thr glu ser gly leu val gly leu leu glu  
5029/1771  
TTG TAC GAG ACG GTT AAT GAA GTC TAC AAG  
leu tyr glu thr val asn glu val tyr lys  
5089/1791  
GAT TTC CGG AAG CTG ACC TCC ACT CAC GAC  
asp phe arg lys leu thr ser thr his asp  
5149/1811  
AAC AAG GAC CAT AAG AGG ATG TTT GGG ACC  
asn lys asp his lys arg met phe gly thr  
5209/1831  
TTT GGG GAT TTG GAT GAG CAG GAG TTC GTG  
phe gly asp leu asp glu gln glu phe val  
5269/1851  
GAG ATC TCA CAT AGA CTA GAG GGA TAT TAT  
glu ile ser his arg leu glu gly phe tyr  
5329/1871  
GTG ATA AAA GAC TCT ACT CCA GTG GAC AAA  
val ile lys asp ser thr pro val asp lys

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5359/1881  
ACC AAG TTG GAT CCT AAC AAG GCC TAC ATT CAG ATC ACT TTT GTG GAG CCT TAC TTT GAT  
thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro tyr phe asp  
5419/1901  
GAA TAT GAG ATG AAA GAC CGG GTG ACC TAC TTC GAG AAG AAT TTC AAC CTC CGG AGG TTC  
glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu arg arg phe  
5479/1921  
ATG TAC ACC ACC CCC TTC ACC CTG GAG GGG AGA CCC CGG GGC GAG CTT CAT GAG CAA CAC  
met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his glu gln his  
5539/1941  
CGC AGA AAC ACC GTG CTC ACC ACC ATG CAC GCC TTC CCC TAC ATC AAG ACC AGG ATC CGA  
arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr arg ile arg  
5599/1961  
GTC AGC CAG AAA GAG GAG TTC GTT TTG ACT CCG ATT GAG GTT GCC ATT GAA GAT ATG AAG  
val ser gln lys glu glu phe val leu thr pro ile glu val ala ile glu asp met lys  
5659/1981  
AAG AAG ACC CTG CAG TTA GCC GTG GCC ACT CAC CAG GAG CCC CCT GAT GCA AAG ATG CTG  
lys lys thr leu gln leu ala val ala thr his gln glu pro pro asp ala lys met leu  
5719/2001  
CAA ATG GTA CTG CAG GGC TCT GTA GGA GCC ACT GTA AAT CAG GGA CCA CTG GAG GTG GCC  
gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu glu val ala  
5779/2021  
CAA GTG TTC TTG GCT GAA ATT CCA GCT GAC CCA AAG CTC TAC CGA CAT CAC AAC AAG CTG  
gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his asn lys leu  
5839/2041  
AGG TTG TGC TTC AAG GAG TTC ATA ATG CGA TGC GGA GAG GCC GTG GAG AAG AAC AGG CGA  
arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys asn arg arg  
5899/2061  
CTC ATC ACC GCA GAG CAG CGG GAG TAC CAG CAG GAG CTG AAG AAG AAC TAC AAC AAG CTG  
leu ile thr ala glu gln arg glu tyr gln gln glu leu lys lys asn tyr asn lys leu  
5959/2081  
AGA GAC AGC CTC AGG CCC ATG ATT GAG CGG AAA ATC CCA GAG CTC TAC AAG CCC ATA TTC  
arg asp ser leu arg pro met ile glu arg lys ile pro glu leu tyr lys pro ile phe  
6019/2101  
AGA GTT GAC AGT CAG AAG AGG GAC TCT TTC CAC AGA TCT AGT TTC AGG AAA TGT GAA ACC  
arg val asp ser gln lys arg asp ser phe his arg ser ser phe arg lys cys glu thr  
6079/2121  
CAG TTG TCA CAG GGC AGC TGA AAA AAG CCA CCT TTG CCG GTG ACG ACT GGG GCC CCA CTA  
gln leu ser gln gly ser OPA  
6139/2141  
CTG GGA AGG ACT CGC TGG

F. mouse CLASP-7 cDNA Sequence

1. Fragment 1

1/1  
CGC CGT CGG GGG CCC CAG GAT CGA GGC TAT AGT GGG GAT GAT GCC TGC AGC TTC TCT AGC  
arg arg arg gly pro gln asp arg gly tyr ser gly asp asp ala cys ser phe ser ser  
61/21  
TTC CGC CGC GCC AGC TTA ACT CTC ACC AAC TTT TTC AAA CAG GAG CCA GAA CGG CTC AGT  
phe arg pro ala thr leu thr val thr asn phe phe lys gln glu ala glu arg leu ser  
91/31

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Figure 4 (30 of 35)

121/41  
 GAT GAA GAC CTT TTC AAG TTT CTG GCC GAC ATG CGG CGA CCA TCA TCC CTG CTG AGG CGA  
 asp glu asp leu phe lys phe leu ala asp met arg arg pro ser ser leu leu arg arg  
 181/61  
 211/71  
 TTG CGC CCT GTG ACA GCT CAG CTC AAG CTT GAC ATC TCC CCG GCC CCC GAG AAC CTG CAC  
 leu arg pro val thr ala gln leu lys leu asp ile ser pro ala pro glu asn leu his  
 241/81  
 271/91  
 TTC TGC CTG TCC CCT GAC TTA CTT CAT GTC AAG CCC TAC CCT GAC CCC AGG GGA CGS CCC  
 phe cys leu ser pro asp leu leu his val lys pro tyr pro asp pro arg gly arg pro  
 301/101  
 331/111  
 ACC AAG GAG ATC CTG GAG TTC CCT GCC CGC GAG GTC TAC GCC CCC CAT TCC TGT TAC AGG  
 thr lys glu ile leu glu phe pro ala arg glu val tyr ala pro his ser cys tyr arg  
 361/121  
 391/131  
 AAC CTG CTC TTC GTG TAC CCA CAC AGC CTC AAT TTC AGC AGT CGC CAG GGC TCT GTG CGC  
 asn leu leu phe val tyr pro his ser leu asn phe ser ser arg gln gly ser val arg  
 421/141  
 451/151  
 AAC CTG GCT GTG CGG ATC CAG TAC ATG GCC GGT GAA GAC CAG AGC CAG GCC TTG CCG GTC  
 asn leu ala val arg ile gln tyr met ala gly glu asp gln ser gln ala leu pro val  
 481/161  
 511/171  
 ATC TTT GGG AAA TCT AGC TGC AGC GAA TTC ACC CGA GAG GCC TTC ACA CCA GTG GTC TAT  
 ile phe gly lys ser ser cys ser glu phe thr arg glu ala phe thr pro val val tyr  
 541/181  
 571/191  
 CAC AAC AAG TCT CCT GAA TTC TAC GAG GAA TTC AAG CTA CGA CTT CCT GCC TGC GTG ACC  
 his asn lys ser pro glu phe tyr glu glu phe lys leu arg leu pro ala cys val thr  
 601/201  
 631/211  
 GAG AAC CAT CAC CTC TTT TTT ACC TTC TAC CAT GTC AGC TGC CAG CCC CGS CCA GGA ACA  
 glu asn his his leu phe phe thr phe tyr his val ser cys gln pro arg pro gly thr  
 661/221  
 691/231  
 CCC TTG GAG AGC CCT GTG GGC TTC ACT TGG ATC CCT CTG TTA CAA CAT GGC CGC CTG AGG  
 ala leu glu thr pro val gly phe thr trp ile pro leu leu gln his gly arg leu arg  
 721/241  
 751/251  
 ACT GGT CCC TTC TGC CTG CCC GTG TCC GTG GAC CAG CCT CCA CCC AGC TAC TCG GTC CTG  
 thr gly pro phe cys leu pro val ser val asp gln pro pro pro ser tyr ser val leu  
 781/261  
 811/271  
 ACC CCA GAT GTA GCG CTG CCT GGC ATG CGC TGG GTG GAC GGC CAC AAG GGC GTG TTC AGT  
 thr pro asp val ala leu pro gly met arg trp val asp gly his lys gly val phe ser  
 841/281  
 871/291  
 GTG GAG CTC ACC GCC GTG TCG TCC GTG CAC CGC CAG GAC CCC CAC TTG GAT AAG TTC TTC  
 val glu leu thr ala val ser ser val his pro gln asp pro his leu asp lys phe phe  
 901/301  
 931/311  
 ACG CTG GTA CAT GTT CTA GAG GAA GGG ATC TTT CCG TTC CGA CTC AAG GAG ACA GTG CTG  
 thr leu val his val leu glu glu gly ile phe pro phe arg leu lys glu thr val leu  
 961/321  
 991/331  
 AGC GAA GGC ACT ATG GAG CAG GAG TTG CGA GCC AGC CTG GCA GCC CTG CGC CTT GCC AGC  
 ser glu gly thr met glu gln glu leu arg ala ser leu ala ala leu arg leu ala ser  
 1021/341  
 1051/351  
 CCA GAG CCC CTA GTA GCC TTT TCC CAC CTC GTG CTA GAC AAG CTT GTC CGC TTG GTT GTG  
 pro glu pro leu val ala phe ser his leu val leu asp lys leu val arg leu val val

1081/361  
 CGG CCA CCC ATC ATT TGT GGC CAG ATG GTG  
 arg pro pro ile ile cys gly gln met val  
 1141/381  
 GCT CAT GTA GCC AGC CTT GTG CAC CGG AAC  
 ala his val ala ser leu val his arg asn  
 1201/401  
 TGC CCA CTG CTG GCC TCC TAT GTC CAC TAC  
 cys pro leu leu ala ser tyr val his tyr  
 1261/421  
 CTG CCA GGC GAA GCC CCT CCA GCA ACT GTG  
 leu pro gly glu ala pro pro ala thr val  
 1321/441  
 CGC CCC GCC AGC CTG TAC CTG GCA CGG TCT  
 arg pro ala ser leu tyr leu ala arg ser  
 1381/461  
 GCT GTG GTC CCT GGC TCT GTG GAC GAT GAG  
 ala val val pro gly ser val asp asp glu  
 1441/481  
 GAT CGC TCA CAC TCC TGG GTG AAT TCT GCT  
 asp arg ser his ser trp val asn ser ala  
 1501/501  
 CGG CGG GTG CCC CCA TAC TGT GGG GCT GAT  
 arg arg val pro pro tyr cys gly ala asp  
 1561/521  
 CTG CAG TGG GTG GTG AGC GGC AGT GCG GTT  
 leu gln trp val val ser gly ser ala val

1111/371  
 AAC CTG GGT CGA GGG GCC TTT GAA GCT ATG  
 asn leu gly arg gly ala phe glu ala met  
 1171/391  
 CTG GAG GCT GTC CAA GAC TCC CGT GGC CAC  
 leu glu ala val gln asp ser arg gly his  
 1231/411  
 GCC TTT CGC CTC CCT GGT GGT GAC CTC AGC  
 ala phe arg leu pro gly gly asp leu ser  
 1291/431  
 CAG GCT GCC ACA CTG GCC CGT GGC TCT GGT  
 gln ala ala thr leu ala arg gly ser gly  
 1351/451  
 AAG AGC ATC AGC AGC AGC AAC CCT GAC CTG  
 lys ser ile ser ser ser asn pro asp leu  
 1411/471  
 GTG TCC CGC ATC CTA GCC AGC AAG GGT GTC  
 val ser arg ile leu ala ser lys gly val  
 1471/491  
 TAT GCT CCG GGA GGC AGC AAG GCT GTG CTG  
 tyr ala pro gly gly ser lys ala val leu  
 1531/511  
 CCC AGA CAG CTG CTG CAC GAG GAG CTG GCT  
 pro arg gln leu leu his glu glu leu ala

## 2. mouse CLASP-7 cDNA fragment 2

1/1  
 ATG GTA AAA AGC ATG GAG CTC CAT CTG CTT  
 Met val lys ser met glu leu his leu leu  
 61/21  
 CTG CGC TTC CTT GGG CGC TTC CTG GAT GAC  
 leu arg phe pro gly arg phe leu asp asp  
 121/41  
 GAA GTC ATC ACC AGA GTC CAT AAG GAC ATG  
 glu val ile thr arg val his lys asp met  
 181/61  
 GCT TTC TTC CTC AGT GAC CTC CTG TCC ATA  
 ala phe leu ser asp leu leu ser ile  
 241/81  
 CGC GCT CAC TAC AAG CAG GTG GCC ACT CGG  
 arg ala his tyr lys gln val ala thr arg  
 301/101  
 CTC ACA CTA CGA ATG GAC TTC ACC CGC ATC  
 leu thr leu arg met asp phe thr arg ile  
 311/11  
 CTG GGC CAG CGA CTG GAC ACT CCC CGC AAG  
 leu gly gln arg leu asp thr pro arg lys  
 91/31  
 ATT GCC GCC CTG GTG GCT TCC GTG GGC CTG  
 ile ala ala leu val ala ser val gly leu  
 151/51  
 AAG CTA GCT GAA CGC CTC AAC GCT AGC CTG  
 lys leu ala glu arg leu asn ala ser leu  
 211/71  
 GCG GAC CGA GGC TAC ATT TTC AGC CTG GTA  
 ala asp arg gly tyr ile phe ser leu val  
 271/91  
 CTC CAG TCT GCC CCC AAC CCA ACT GCA CTG  
 leu gln ser ala pro asn pro thr ala leu  
 331/111  
 CTG TGT AGC CAT GAG CAC TAT GTG ACC CTT  
 leu cys ser his glu his tyr val thr leu



# 33/95

361/121  
AAC CTC CCC TGT TGC CCC CTG TCG CCC CCA GCA TCC CCG TCC CCC TCG GTG TCC TCC ACT  
asn leu pro cys cys pro leu ser pro pro ala ser pro ser pro ser val ser ser thr  
421/141  
ACC TCC CAG AGC TCC ACC TTC TCC AGC CAG GCC CCC GAT CCG AAG GTG ACC AGC ATG TTC  
thr ser gln ser ser thr phe ser ser gln ala pro asp pro lys val thr ser met phe  
481/161  
GAG CTG AGC GGG CCC TTC AGG CAG CAG CAC TTC CTG TCC GGA CTC CTG CTG ACA GAG CTG  
glu leu ser gly pro phe arg gln gln his phe leu ser gly leu leu leu thr glu leu  
541/181  
GCC CTG GCC CTG GAT CCG GAA GCT GAG GGG GCA TCC CTT TTG CAC AAG AAG GCT ATT AGT  
ala leu ala leu asp pro glu ala glu gly ala ser leu leu his lys lys ala ile ser  
601/201  
GCC CTG CAC AGC CTG CTG TGC AGC CAC GAT GTT GAC TCC CGC TAC GCA GAA GCT ACC GTG  
ala val his ser leu leu cys ser his asp val asp ser arg tyr ala glu ala thr val  
661/221  
AAC GCC AAG GTG GCC GAG CTG TAC CTG CCC CTC CTC TCC CTT  
asn ala lys val ala glu leu tyr leu pro leu leu ser leu

## 3. mouse CLASP-7 cDNA fragment 3

1/1  
GAA ATG GAA CAT GAA GCT CTG GTG GAC GGA AAC CTG GCG ACA GAG GCC AGC CTG GTG GTT  
glu met glu his glu ala leu val asp gly asn leu ala thr glu ala ser leu val val  
61/21  
CTG GAC ACG CTG GAG ACC ATC GTG CAG ACA GTG ATG CTG TCC GAG GCC CGT GAG AGC ATC  
leu asp thr leu glu thr ile val gln thr val met leu ser glu ala arg glu ser ile  
121/41  
CTG AGT GCC CTG CTG AAA GTT GTC CTC TAC AGT CTT GGG AGC GCC CAG AGT GCC CTG TTC  
leu ser ala val leu lys val val leu tyr ser leu gly ser ala gln ser ala leu phe  
181/61  
CTG CAG CAT GGC CTG GCC ACC CAG CGG GCC CTC GTG TCC AAG TTT CCG GAG CTG CTT TTC  
leu gln his gly leu ala thr gln arg ala leu val ser lys phe pro glu leu leu phe  
241/81  
GAG GAA GAC ACG GAG CTT TGT GCC CAG CTG TGC CTG AGA CTT CTG CGA CAC TGT GGC AGC  
glu glu asp thr glu leu cys ala asp leu cys leu arg leu leu arg his cys gly ser  
301/101  
CGC ATC AGC ACC ATC CGC ATG CAC GCC AGC GCC TCC CTC TAC CTG CTT ATG CGC CAG AAC  
arg ile ser thr ile arg met his ala ser ala ser leu tyr leu leu met arg gln asn  
361/121  
TTC GAG ATT GGC CAT AAC TTT GCC CGT GTG AAG ATG CTG GTG ACC ATG TCT CTG TCG TCC  
phe glu ile gly his asn phe ala arg val lys met leu val thr met ser leu ser ser  
421/141  
CTT GTG GGG ACA ACT CAG AAC TTT AGT GAA GAG CAT TTG AGA AAG TCC CTC AAG ACC ATC  
leu val gly thr thr gln asn phe ser glu glu his leu arg lys ser leu lys thr ile  
481/161  
CTG ACC TAC GCA GAG GAG GAC ATA GGG CTG AGG GAC AGC ACC TTC GCT GAG CAG GTC CAG  
leu thr tyr ala glu glu asp ile gly leu arg asp ser thr phe ala glu gln val gln

541/181  
 GAC CTC ATG TTC AAC CTG CAC ATG ATC CTG ACA GAC ACG GTG AAG ATG AAG GAA CAC CAG  
 asp leu met phe asn leu his met ile leu thr asp thr val lys met lys glu his gln  
 601/201  
 GAG GAC CCT GAG ATG CTC ATG GAC CTC ATG TAC AGA ATT GCT CGG GGA TAC CAA GGC TCT  
 glu asp pro glu met leu met asp leu met tyr arg ile ala arg gly tyr gln gly ser  
 661/221  
 CCA GAC CTG CGG CTG ACA TGG CTG CAG AAC ATG GCT GGC AAA CAT GCA GAG CTG GGC AAT  
 pro asp leu arg leu thr trp leu gln asn met ala gly lys his ala glu leu gly asn  
 721/241  
 CAT GCA GAG GCT GCC CAG TGC ATG GTC CAC GCC GCT GCC CTG GTG GCC GAA TAC CTT GCC  
 his ala glu ala ala gln cys met val his ala ala ala leu val ala glu tyr leu ala  
 781/261  
 CTC CTC GAG GAC AGT CGC CAC CTG CCT GTG GGC TGT GTG TOC TTC CAG AAT GTC TCA TCC  
 leu leu glu asp ser arg his leu pro val gly cys val ser phe gln asn val ser ser  
 841/281  
 AAC GTG CTG GAG GAG TCT GCC ATC TCT GAT GAC ATC CTG TCG CCA GAT GAG GAG GGC TTC  
 asn val leu glu glu ser ala ile ser asp asp ile leu ser pro asp glu glu gly phe  
 901/301  
 TGC TCT GGG AAG AAC TTC ACA GAA CTG GGT CTG GTG GGG CTG CTG GAG CAG GCG GCC GGC  
 cys ser gly lys asn phe thr glu leu gly leu val gly leu leu glu gln ala ala gly  
 961/321  
 TAC TTC ACC ATG GGT GGT CTG TAT GAA GCG GTG AAC GAA GTC TAC AAA AAC CTT ATC CCC  
 tyr phe thr met gly gly leu tyr glu ala val asn glu val tyr lys asn leu ile pro  
 1021/341  
 ATC CTT GAA GCC CAC AGA GAC TAC AAG AAG CTG GCT GCG GTG CAC GGG AAA CTG CAG GAG  
 ile leu glu ala his arg asp tyr lys lys leu ala ala val his gly lys leu gln glu  
 1081/361  
 GCC TTC ACC AAG ATT ATG CAC CAG AGC TCT GGC TGG GAG CGT GTA TTT GGG ACA TAT TTC  
 ala phe thr lys ile met his gln ser ser gly trp glu arg val phe gly thr tyr phe  
 1141/381  
 CGA GTG GGC TTC TAT GGC ACA CGA TTT GGT GAC CTG GAT GAA CAA GAG TTT GTG TAC AAG  
 arg val gly phe tyr gly thr arg phe gly asp leu asp glu gln glu phe val tyr lys  
 1201/401  
 GAA CCG TCA ATC ACG AAG CTT GCA GAG ATC TCA CAC CGG CTG GAG GAG TTC TAT ACG GAA  
 glu pro ser ile thr lys leu ala glu ile ser his arg leu glu glu phe tyr thr glu  
 1261/421  
 AGG TTC GGG GAT GAT GTG GTA GAG ATC ATC AAA GAT TCT AAC CCA GTG GAC AAG TCC AAG  
 arg phe gly asp asp val val glu ile ile lys asp ser asn pro val asp lys ser lys  
 1321/441  
 CTG GAC CCA CAG AAG CGC TAC ATA CAG ATA ACC TAT GTG GAG CCA CAT TTC GAC ACT TAT  
 leu asp pro gln lys ala tyr ile gln ile thr tyr val glu pro his phe asp thr tyr  
 1381/461  
 GAG CTC AAG GAT CGG GTG ACC TAC TTC GAT CGG AAC TAT GGG CTG CGG GCC TTC CTC TTC  
 glu leu lys asp arg val thr tyr phe asp arg asn tyr gly leu arg ala phe leu phe  
 1441/481  
 TGC ACA CCC TTC ACA CCA GAT GGA CGT GCG CAC GGA GAG TTG GCC GAA CAG CAC AAA CGC  
 cys thr pro phe thr pro asp gly arg ala his gly glu leu ala glu gln his lys arg

j<sub>b</sub>

Figure 7 (34 of 35)

35/95

1501/501	1531/511
AAG ACG CTG CTG AGC ACG GAG CAT GCC TTT	CCC TAC ATC AAG ACA CGC ATC CGA GTG TGC
lys thr leu leu ser thr glu his ala phe	pro tyr ile lys thr arg ile arg val cys
1561/521	1591/531
CAC CGT GAG GAG ACA GTG CTG ACA CCA GTG	GAG GTG GCC ATT GAG GAC ATG CAG AAG AAG
his arg glu glu thr val leu thr pro val	glu val ala ile glu asp met gln lys lys
1621/541	1651/551
ACC CGG GAG CTG GCC TTT GCC ACC GAG CAG	GAC CCT CCA GAT GCC AAG ATG CTG CAG ATG
thr arg glu leu ala phe ala thr glu gln	asp pro pro asp ala lys met leu gln met
1681/561	1711/571
GTT CTC CAG GGT TCT GTG GGA CCC ACT GTG	AAC CAG GGT CCC TTG GAA GTG GCC CAG GTG
val leu gln gly ser val gly pro thr val	asn gln gly pro leu glu val ala gln val
1741/581	1771/591
TTT TTG TCA GAG ATC CCA GAA GAT CCC AAG	CTC TTC CGA CAT CAC AAC AAA CTC CGG CTC
phe leu ser glu ile pro glu asp pro lys	leu phe arg his his asn lys leu arg leu
1801/601	1831/611
TGC TTC AAG GAT TTC TGC AAA AAG TGC GAG	GAT GCA CTG AGA AAG AAC AAG GCC CTG ATT
cys phe lys asp phe cys lys lys cys glu	asp ala leu arg lys asn lys ala leu ile
1861/621	1891/631
GGC CCA GAC CAG AAG GAG TAC CAC CGG GAG	CTG GAG CGT CAC TAT AGC CGC CTG CGG GAG
gly pro asp gln lys glu tyr his arg glu	leu glu arg his tyr ser arg leu arg glu
1921/641	1951/651
GCT CTG CAG CCT CTG CTT ACC CAA COT CTG	CCC CAG CTG CTG GCA CCA AGT TCC ACC AGC
ala leu gln pro leu leu thr gln arg leu	pro gln leu leu ala pro ser ser thr ser
1981/661	2011/671
CTC AGG AGC TCC ATG AAC AGA TCA AGT TTC	AGG AAG GCT GAC CTC TGA CAA GGC TAA GAG
leu arg ser ser met asn arg ser ser phe	arg lys ala asp leu OPA
2041/681	2071/691
CCA CAC CCA GAA GAC CAG CAC CCA CAC TGA	AAA

GTGCGCGTCGCGCAGCAGCC -1

1/1  
 ATG GCC GAG CGC CGC GCC TTC GCC CAG AAG ATC AGC AGA ACG GTG GCA GCC GAA GTT AGG  
 Met ala glu arg arg ala phe ala gln lys ile ser arg thr val ala ala glu val arg  
 61/21  
 AAG CAG ATC TCC GGA CAA TAT AGT GGT TCT CCC CAA CTG CTC AAA AAC CTT AAT ATT GTT  
 lys gln ile ser gly gln tyr ser gly ser pro gln leu leu lys asn leu asn ile val  
 121/41  
 GGC AAT ATA TCC CAT CAC ACC ACA GTG CCC CTT ACC GAA GCA GTA GAT CCA GTG GAT TTG  
 gly asn ile ser his his thr thr val pro leu thr glu ala val asp pro val asp leu  
 181/61  
 GAA GAT TAC CTC ATT ACT CAT CCT TTG GCT GTG GAT TCT GGG CCT TTA CGG GAT TTG ATT  
 glu asp tyr leu ile thr his pro leu ala val asp ser gly pro leu arg asp leu ile  
 241/81  
 GAA TTT CCT CCA GAT GAT ATT GAA GTT GTT TAT AGT CCT CGG GAC TGC AGA ACT CTT GTT  
 glu phe pro pro asp asp ile glu val val tyr ser pro arg asp cys arg thr leu val  
 301/101  
 TCA GCT GTA CCT GAA GAA AGT GAA ATG GAT CCA CAT GTT AGA GAC TGT ATA AGA AGT TAT  
 ser ala val pro glu glu ser glu met asp pro his val arg asp cys ile arg ser tyr  
 361/121  
 ACA GAA GAC TGG GCA ATT GTC ATC AGA AAA TAT CAT AAA TTG GGA ACA GGA TTT AAT CCC  
 thr glu asp trp ala ile val ile arg lys tyr his lys leu gly thr gly phe asn pro  
 421/141  
 AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA AAA GGT TTG CCA AAA CAA GTT TTT GAA TCT  
 asn thr leu asp lys gln lys glu arg gln lys gly leu pro lys gln val phe glu ser  
 481/161  
 GAT GAA GCT CCA GAT GGC AAC AGC TAC CAG GAT GAT CAA GAT GAC CTT AAA AGA CGT TCA  
 asp glu ala pro asp gly asn ser tyr gln asp asp gln asp asp leu lys arg arg ser  
 541/181  
 ATG TCA ATA GAT GAT ACC CCA AGG GGT AGC TGG GCC TGT AGT ATC TTT GAC TTG AAA AAT  
 met ser ile asp asp thr pro arg gly ser trp ala cys ser ile phe asp leu lys asn  
 601/201  
 TCA CTT CCT GAT GCT TTG CTT CCC AAT TTA CTT GAT CGA ACT CCA AAT GAA GAA ATA GAC  
 ser leu pro asp ala leu leu pro asn leu leu asp arg thr pro asn glu glu ile asp  
 661/221  
 CGT CAG AAT GAT GAC CAA AGG AAA TCA AAC CGT CAC AAA GAA CTT TTT GCT TTG CAT CCA  
 arg gln asn asp asp gln arg lys ser asn arg his lys glu leu phe ala leu his pro  
 721/241  
 TCA CCA GAT GAG GAA GAA CCA ATA GAA CGG CTT AGT GTT CCT GAT ATA CCC AAA GAA CAT  
 ser pro asp glu glu glu pro ile glu arg leu ser val pro asp ile pro lys glu his  
 781/261  
 TTT GGT CAA AGA CTT CTT GTA AAA TGC TTA TCA CTC AAG TTT GAA ATT GAA ATT GAA CCC  
 phe gly gln arg leu leu val lys cys leu ser leu lys phe glu ile glu ile glu pro  
 841/281  
 ATT TTT GCA AGT TTG GCT TTA TAT GAT GTC AAG GAA AAG AAA AAG ATT TCA GAA AAC TTT  
 ile phe ala ser leu ala leu tyr asp val lys glu lys lys lys ile ser glu asn phe  
 901/301  
 TAT TTT GAC CTT AAT TCT GAG CAG ATG AAA GGG TTG TTA CGT CCA CAT GTA CCA CCT GCT  
 tyr phe asp leu asn ser glu gln met lys gly leu leu arg pro his val pro pro ala  
 961/321  
 GCC ATT ACT ACC CTG GCA AGA TCA GCA ATT TTT TCT ATC ACT TAT CCT TCC CAA GAT GTT  
 ala ile thr thr leu ala arg ser ala ile phe ser ile thr tyr pro ser gln asp val

1021/341  
TTT CTT GTA ATA AAG CTA GAA AAA GTC CTA CAG CAA GGA GAC ATT GGA GAG TGT GCA GAA  
phe leu val ile lys leu glu lys val leu gln gln gly asp ile gly glu cys ala glu  
1081/361  
CCA TAT ATG ATT TTC AAA GAA GCA GAT GCC ACC AAG AAT AAA GAA AAA CTG GAG AAA CTG  
pro tyr met ile phe lys glu ala asp ala thr lys asn lys glu lys leu glu lys leu  
1141/381  
AAG AGT CAA GCA GAT CAG TTT TGC CAA AGA CTT GGG AAA TAT CGC ATG CCT TTT GCT TGG  
lys ser gln ala asp gln phe cys gln arg leu gly lys tyr arg met pro phe ala trp  
1201/401  
ACT GCA ATC CAT TTA ATG AAT ATT GTT AGC AGT GCT GGG AGT TTG GAA AGA GAT TCT ACA  
thr ala ile his leu met asn ile val ser ser ala gly ser leu glu arg asp ser thr  
1261/421  
GAA GTA GAA ATC AGT ACT GGA GAA CGA AAA GGG TCT TGG TCA GAG AGG AGG AAT TCT AGT  
glu val glu ile ser thr gly glu arg lys gly ser trp ser glu arg arg asn ser ser  
1321/441  
ATT GTT GGC AGA CGA TCA CTT GAA AGG ACA ACA AGT GGA GAT GAT GCT TGT AAC TTG ACG  
ile val gly arg arg ser leu glu arg thr thr ser gly asp asp ala cys asn leu thr  
1381/461  
AGC TTT CGA CCA GCT ACT CTC ACA GTG ACA AAT TTT TTT AAG CAG GAA GGA GAC CGC TTA  
ser phe arg pro ala thr leu thr val thr asn phe phe lys gln glu gly asp arg leu  
1441/481  
AGT GAT GAA GAT CTC TAC AAA TTC CTT GCT GAT ATG AGA AGG CCA TCT TCT GTC TTA CGG  
ser asp glu asp leu tyr lys phe leu ala asp met arg arg pro ser ser val leu arg  
1501/501  
CGA CTA AGA CCT ATT ACA GCT CAG CTC AAG ATA GAC ATT TCT CCC GCA CCT GAA AAT CCC  
arg leu arg pro ile thr ala gln leu lys ile asp ile ser pro ala pro glu asn pro  
1561/521  
CAT TAT TGC CTA ACT CCG GAG CTG CTT CAA GTG AAG CTT TAC CCT GAC AGT AGA GTT AGA  
his tyr cys leu thr pro glu leu leu gln val lys leu tyr pro asp ser arg val arg  
1621/541  
CCT ACC AGA GAA ATC TTA GAG TTT CCC GCA AGG GAT GTT TAT GTT CCA AAC ACT ACT TAC  
pro thr arg glu ile leu glu phe pro ala arg asp val tyr val pro asn thr thr tyr  
1681/561  
AGA AAT CTT CTC TAC ATA TAC CCT CAG AGT CTT AAT TTT GCC AAT CGT CAA GGT TCT GCT  
arg asn leu leu tyr ile tyr pro gln ser leu asn phe ala asn arg gln gly ser ala  
1741/581  
AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG TAT GGA GAG GAT CCA AGC AAT GCC ATG CCG  
arg asn ile thr val lys val gln phe met tyr gly glu asp pro ser asn ala met pro  
1801/601  
GTA ATC TTT GGT AAA TCT AGC TGT TCA GAA TTT TCA AAG GAA GCC TAT ACA GCC GTA GTA  
val ile phe gly lys ser ser cys ser glu phe ser lys glu ala tyr thr ala val val  
1861/621  
TAT CAT AAG AGC TCT CCT GAT TTT CAT GAA GAA ATC AAG GTT AAG CTT CCT GCT ACT TTA  
tyr his asn arg ser pro asp phe his glu glu ile lys val lys leu pro ala thr leu  
1921/641  
ACT GAC CAT CAT CAC TTG CTT TTT ACT TTT TAT CAT GTT AGT TGT CAA CAA AAA CAA AAT  
thr asp his his his leu leu phe thr phe tyr his val ser cys gln gln lys gln asn  
1981/661  
ACT CCT CTT GAA ACA CCA GTT GGA TAT ACA TGG ATA CCA ATG CTT CAG AAT GGA CGG TTG  
thr pro leu glu thr pro val gly tyr thr trp ile pro met leu gln asn gly arg leu  
2041/681  
AAG ACT GGC CAG TTT TGC TTG CCA GTC TCA TTG GAA AAA CCA CCA CAG GCT TAT TCT GTA  
lys thr gly gln phe cys leu pro val ser leu glu lys pro pro gln ala tyr ser val  
2101/701  
CTG TCT CCT GAG GTT CCT CTA CCT GGC ATG AAA TGG GTA GAT AAT CAC AAA GGT GTT TTT  
leu ser pro glu val pro leu pro gly met lys trp val asp asn his lys gly val phe

2161/721  
AAT GTT GAA GTT GTT GCT GTT TCG TCT ATC  
asn val glu val val ala val ser ser ile  
2221/741  
TTT GCT CTG GTC AAT GCT CTG GAT GAA CAC  
phe ala leu val asn ala leu asp glu his  
2281/761  
ATC ATG GAA AAT AAC TTA GAA AAT GAA TTG  
ile met glu asn asn leu glu asn glu leu  
2341/781  
CAG CTG GAA CCA GTG GTC CGA TTT CTT CAT  
gln leu glu pro val val arg phe leu his  
2401/801  
ATT AGA CCT CCT GTC ATT GCT GGC CAA ATA  
ile arg pro pro val ile ala gly gln ile  
2461/821  
ATG GCA TCA ATT ATA AAT CGA CTT CAC AAA  
met ala ser ile ile asn arg leu his lys  
2521/841  
AGA AAC AGC CTT CTT GCA TCA TAT ATT CAT  
arg asn ser leu leu ala ser tyr ile his  
2581/861  
AAT TCA TCA TCA CCA GGT CCT GGG GGT TTG  
asn ser ser ser pro gly pro gly gly leu  
2641/881  
AGA TCT GCG GTG AGA CCT GCA AGC CTT AAT  
arg ser ala val arg pro ala ser leu asn  
2701/901  
AAT CCA GAT ATA TCT GGG ACT CCC ACG TCA  
asn pro asp ile ser gly thr pro thr ser  
2761/921  
AGT AAG GGT TTA GAT CGC TCC AAT TCC TGG  
ser lys gly leu asp arg ser asn ser trp  
2821/941  
TGG GGA TCC AAC CCC AGT CCA AGT GCA GAA  
trp gly ser asn pro ser pro ser ala glu  
2881/961  
CGT ATG TCT TCG CAC ACA GAG ACG TCA AGT  
arg met ser ser his thr glu thr ser ser  
2941/981  
ACT AAA AAG CTT TTT CAC GAG GAG CTG GCT  
thr lys lys leu phe his glu glu leu ala  
3001/1001  
CGG GAA TCA GCT TTG CAA CAA GCC TGG TTC  
arg glu ser ala leu gln gln ala trp phe  
3061/1021  
CAC CAT TTA TAC TTT AAT GAT AAA CTT GAG  
his his leu tyr phe asn asp lys leu glu  
3121/1041  
TTC ATG GAT GAC ATT GCA GCT CTT GTC AGC  
phe met asp asp ile ala ala leu val ser  
3181/1061  
CAG AAG GAC ACA GAA ATG GTT GAG AGA CTC  
gln lys asp thr glu met val glu arg leu  
3241/1081  
CTG TTG TCT GTT ATG GAC AGA GGA TTT GTT  
leu leu ser val met asp arg gly phe val

2191/731  
CAT ACA CAA GAT CCT TAT CTT GAC AAA TTT  
his thr gln asp pro tyr leu asp lys phe  
2251/751  
CTG TTC CCA GTC CGA ATT GGG GAC ATG CGA  
leu phe pro val arg ile gly asp met arg  
2311/771  
AAG AGC AGT ATT TCA GCA CTG AAT TCA TCC  
lys ser ser ile ser ala leu asn ser ser  
2371/791  
CTT CTG CTA GAT AAA CTG ATA CTT TTA GTT  
leu leu leu asp lys leu ile leu leu val  
2431/811  
GTT AAC CTA GGT CAA GCA TCT TTT GAA GCC  
val asn leu gly gln ala ser phe glu ala  
2491/831  
AAC TTG GAA GGA AAT CAT GAC CAG CAT GGC  
asn leu glu gly asn his asp gln his gly  
2551/851  
TAT GTT TTC CGC CTA CCA AAT ACT TAC CCT  
tyr val phe arg leu pro asn thr tyr pro  
2611/871  
GGA GGA TCA GTG CAT TAT GCC ACA ATG GCT  
gly gly ser val his tyr ala thr met ala  
2671/891  
TTA AAT CGT TCT CGA AGC CTT AGT AAT AGC  
leu asn arg ser arg ser leu ser asn ser  
2731/911  
CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG  
pro asp asp glu val arg ser ile ile gly  
2791/931  
GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA  
val asn thr gly gly pro lys ala ala pro  
2851/951  
TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT  
ser thr gln ala met asp arg ser cys asn  
2911/971  
TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA  
phe leu gln thr leu thr gly arg leu pro  
2971/991  
TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT  
leu gln trp val val cys ser gly ser val  
3031/1011  
TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG  
phe phe glu leu met val lys ser met val  
3091/1031  
GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT  
ala pro arg lys ser arg phe pro glu arg  
3151/1051  
ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT  
thr ile ala ser asp ile val ser arg phe  
3211/1071  
AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT  
asn thr ser leu ala phe phe leu asn asp  
3271/1091  
TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG  
phe ser leu ile lys ser cys tyr lys gln

3301/1101  
GTG TCT TCA AAG CTT TAC TCA TTA CCG AAT  
val ser ser lys leu tyr ser leu pro asn  
3361/1121  
TTT CTA CGA ATC ATC TGC AGT CAT GAG CAC  
phe leu arg ile ile cys ser his glu his  
3421/1141  
CTT ACT CCA CCT GCA TCT CCA TCA CCT TCT  
leu thr pro pro ala ser pro ser pro ser  
3481/1161  
TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT  
phe ser thr asn val gln asp gln lys ile  
3541/1181  
CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG  
arg gln gln his tyr leu ala gly leu val  
3601/1201  
GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG  
asp ala glu gly leu phe gly leu his lys  
3661/1221  
TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT  
ser ser his asp ser asp pro arg tyr ser  
3721/1241  
TTG TAT CTA CCT CTG ATT GGT ATT ATC ATG  
leu tyr leu pro leu ile gly ile ile met  
3781/1261  
GAA ACT CAC AAT CAA CGA GGA AGA CCA ATT  
glu thr his asn gln arg gly arg pro ile  
3841/1281  
AGC GGA AGT ATG ATA AGC CAG ACC GTT GCC  
ser gly ser met ile ser gln thr val ala  
3901/1301  
CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG  
leu thr arg pro gly ser phe leu leu thr  
3961/1321  
TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC  
ser ala glu ser ser arg ser leu leu ile  
4021/1341  
GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT  
glu thr val leu gln lys trp phe thr asp  
4081/1361  
GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT  
asp leu leu tyr leu cys val ser cys phe  
4141/1381  
ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA  
met asn ser leu thr phe lys lys ser lys  
4201/1401  
CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG  
leu gly ser ile gly ala arg gln glu met  
4261/1421  
AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA  
ser pro ser gly ser ala phe gly ser gln  
4321/1441  
CAC TGG CGT CAA AAC ACA GAG AAG CTT GAC  
his trp arg gln asn thr glu lys leu asp  
4381/1461  
CTG ATT GAT GGA AAC CTG GCT ACA GAA GCA  
leu ile asp gly asn leu ala thr glu ala

3331/1111  
CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT  
pro ser val leu val ser leu arg leu asp  
3391/1131  
TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA  
tyr val thr leu asn leu pro cys ser leu  
3451/1151  
GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA  
val ser ser ala thr ser gln ser ser gly  
3511/1171  
GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC  
ala asn met phe glu leu ser val pro phe  
3571/1191  
TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT  
leu thr glu leu ala val ile leu asp pro  
3631/1211  
AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC  
lys val ile asn met val his asn leu leu  
3691/1231  
GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG  
asp pro gln ile lys ala arg val ala met  
3751/1251  
GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA  
glu thr val pro gln leu tyr asp phe thr  
3811/1271  
TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG  
cys ile ala thr asp asp tyr glu ser glu  
3871/1291  
ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA  
met ala ile ala gly thr ser val pro gln  
3931/1311  
TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT  
ser thr ser gly arg gln his thr thr phe  
3991/1331  
TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT  
cys leu leu trp val leu lys asn ala asp  
4051/1351  
CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA  
leu ser val leu gln leu asn arg leu leu  
4111/1371  
GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA  
glu tyr lys gly lys lys val phe glu arg  
4171/1391  
GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT  
asp met arg ala lys leu glu glu ala ile  
4231/1411  
GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA  
val arg arg ser arg gly gln leu glu arg  
4291/1431  
GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT  
glu asn leu arg trp arg lys asp met thr  
4351/1451  
AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA  
lys ser arg ala glu ile glu his glu ala  
4411/1471  
AAA CTA ATC ATT TTA GAT ACA TTA GAG ATT  
asn leu ile ile leu asp thr leu glu ile

4441/1481  
GTT GTT CAG ACC GTT TCT GTA ACG GAA TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA  
val val gln thr val ser val thr glu ser lys glu ser ile leu gly gly val leu lys  
4501/1501  
GTG CTA CTA CAC AGC ATG GCC TGT AAC CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT  
val leu leu his ser met ala cys asn gln ser ala val tyr leu gln his cys phe ala  
4561/1521  
ACA CAG AGA GCC TTG GTT TCA AAG TTT CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG  
thr gln arg ala leu val ser lys phe pro glu leu leu phe glu glu glu thr glu gln  
4621/1541  
TGT GCT GAT TTA TGC CTC AGG CTT CTC CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG  
cys ala asp leu cys leu arg leu leu arg his cys ser ser ser ile gly thr ile arg  
4681/1561  
TCA CAC CCC AGT GCC TCC CTT TAC CTA CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC  
ser his pro ser ala ser leu thr leu leu met arg gln asn phe glu ile gly asn asn  
4741/1581  
TTT GCC AGG GTT AAA ATG CAG GTA CCA ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG  
phe ala arg val lys met gln val pro met ser leu ser ser leu val gly thr ser gln  
4801/1601  
AAT TTT AAT GAA GAA TTC TTA AGA CGT TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA  
asn phe asn glu glu phe leu arg arg ser leu lys thr ile leu thr tyr ala glu glu  
4861/1621  
GAT CTG GAA TTG AGG GAA ACA ACA TTT CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC  
asp leu glu leu arg glu thr thr phe pro asp gln val gln asp leu val phe asn leu  
4921/1641  
CAT ATG ATT CTT TCT GAT ACT GTG AAA ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG  
his met ile leu ser asp thr val lys met lys glu his gln glu asp pro glu met leu  
4981/1661  
ATT GAT CTA ATG TAC AGA ATT GCC AAG GGT TAC CAG ACC TCT CCA GAG CGA TTG ACC TGG  
ile asp leu met tyr arg ile ala lys gly tyr gln thr ser pro glu arg leu thr trp  
5041/1681  
TTG CAG AAC ATG GCA GGC AAG CAC TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT  
leu gln asn met ala gly lys his ser glu arg ser asn his ala glu ala ala gln cys  
5101/1701  
CTA GTC CAC TCA GCA GCA CTT GTT GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT  
leu val his ser ala ala leu val ala glu tyr leu ser met leu glu asp arg lys tyr  
5161/1721  
CTT CCT GTG GGA TGT GTA ACA TTT CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG  
leu pro val gly cys val thr phe gln asn ile ser ser asn val leu glu glu ser ala  
5221/1741  
GTC TCA GAT GAT GTG GTA TCT CCA GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT  
val ser asp asp val val ser pro asp glu glu gly ile cys ser gly lys tyr phe thr  
5281/1761  
GAG TCA GGA CTT GTG GGA TTA CTG GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG  
glu ser gly leu val gly leu leu glu gln ala ala ala ser phe ser met ala gly met  
5341/1781  
TAT GAA GCA GTT AAT GAA GTT TAC AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT  
tyr glu ala val asn glu val tyr lys val leu ile pro ile his glu ala asn arg asp  
5401/1801  
GCA AAG AAA CTA TCC ACA ATT CAT GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT  
ala lys lys leu ser thr ile his gly lys leu gln glu ala phe ser lys ile val his  
5461/1821  
CAG AGT ACT GGC TGG GAG CGG ATG TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC  
gln ser thr gly trp glu arg met phe gly thr tyr phe arg val gly phe tyr gly thr  
5521/1841  
AAG TTC GGG GAT TTG GAT GAA CAA GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT  
lys phe gly asp leu asp glu gln glu phe val tyr lys glu pro ala ile thr lys leu



5581/1861  
 GCA GAG ATA TCT CAC AGA TTG GAG GGA TTT  
 ala glu ile ser his arg leu glu gly phe  
 5641/1881  
 GAA GTA ATC AAA GAC TCT AAT CCT GTA GAC  
 glu val ile lys asp ser asn pro val asp  
 5701/1901  
 ATT CAG ATT ACC TAT GTG GAG CCA TAC TTT  
 ile gln ile thr tyr val glu pro tyr phe  
 5761/1921  
 TAT TTC GAC AAA AAT TAC AAT CTT CGT CGA  
 tyr phe asp lys asn tyr asn leu arg arg  
 5821/1941  
 GGC CGT GCC CAT GGG GAA CTT CAT GAA CAA  
 gly arg ala his gly glu leu his glu gln  
 5881/1961  
 CAT GCC TTT CCT TAT ATT AAA ACA AGG GTC  
 his ala phe pro tyr ile lys thr arg val  
 5941/1981  
 ACA CCA ATT GAA GTT GCT ATT GAG GAC ATG  
 thr pro ile glu val ala ile glu asp met  
 6001/2001  
 ACA CAT CAG GAT CCC GCA GAC CCC AAA ATG  
 thr his gln asp pro ala asp pro lys met  
 6061/2021  
 ACC ACA GTG AAT CAG GGG CCT TTG GAA GTT  
 thr thr val asn gln gly pro leu glu val  
 6121/2041  
 GAC CCA AAG CTC TTC AGA CAT CAT AAT AAA  
 asp pro lys leu phe arg his his asn lys  
 6181/2061  
 AGG TGT GAA GAT GCC TTA AGA AAA AAT AAG  
 arg cys glu asp ala leu arg lys asn lys  
 6241/2081  
 CAA AGG GAA TTG GGG AAA CTA TCT TCG CCT TAA  
 gln arg glu leu gly lys leu ser ser pro OCH

5611/1871  
 TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT  
 tyr gly glu arg phe gly glu asp val val  
 5671/1891  
 AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT  
 lys cys lys leu asp pro asn lys ala tyr  
 5731/1911  
 GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC  
 asp thr tyr glu met lys asp arg ile thr  
 5791/1931  
 TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT  
 phe met tyr cys thr pro phe thr leu asp  
 5851/1951  
 TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT  
 phe lys arg lys thr ile leu thr thr ser  
 5911/1971  
 AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA  
 asn val thr his lys glu glu ile ile leu  
 5971/1991  
 CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA  
 gln lys lys thr gln glu leu ala phe ala  
 6031/2011  
 CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC  
 leu gln met val leu gln gly ser val gly  
 6091/2031  
 GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT  
 ala gln val phe leu ser glu ile pro ser  
 6151/2051  
 CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA  
 leu arg leu cys phe lys asp phe thr lys  
 6211/2071  
 AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT  
 ser leu ile gly pro val gln lys glu tyr  
 6271/2091

AGAGGCCCTACAGCCCTAGATCACAGAAAGTCCCTCAGTTATCCAAGCCAGTATTGCTTGTCCCCTGCCACAGAGATTCC  
 TTCAGTCGAATGAGCTTTTCGCAAAATGGATCTCTAAACTGAATGCACTTGTTTTATTTCATCTGCAAAGAGCCATGTATTC  
 AACATCGAGTGTGAAAAGATCTATTGGAAACCAACATGGAATGGAATTCTGGAAATATTATTATTCAATTGAAGAATGCAAGTG  
 GCCAAGAAAATATCAAAATGTAGATTGTTAAACGCTTGAGAATCATGGCTATTGGTTTCTAATGTTCCGGTAACAAGCTGTTA  
 TCTTTTAAGACATTTTAAATGACTCAAAGGTACACTATACATTTACCATTTATTTATACCATAGCTAAGGTTAAAAATTTAT  
 TCACTTTAAGTTCGTATTTTAAATTTATATACCATTTATAGATTCAATTTGGACCCATTAAATGTAGTAATGCTTA  
 TTTTAAAGGTACTAAAAAATATGTGAATGTTTACCTCGTGCAGCCAGGGCCTC

-12 -1  
GACGCGAGGACC

1/1 31/11  
ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG  
Met ala ala ser glu arg arg ala phe ala his lys ile asn arg thr val ala ala glu  
61/21 91/31  
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC  
val arg lys gln val ser arg glu arg ser gly ser pro his ser ser arg arg cys ser  
121/41 151/51  
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT  
ser ser leu gly val pro leu thr glu val val glu pro leu asp phe glu asp val leu  
181/61 211/71  
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT  
leu ser arg pro pro asp ala glu pro gly pro leu arg asp leu val glu phe pro ala  
241/81 271/91  
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC  
asp asp leu glu leu leu leu gln pro arg glu cys arg thr thr glu pro gly ile pro  
301/101 331/111  
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG  
lys asp glu lys leu asp ala gln val arg ala ala val glu met tyr ile glu asp trp  
361/121 391/131  
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC  
val ile val his arg arg tyr gln tyr leu ser ala ala tyr ser pro val thr thr asp  
421/141 451/151  
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA  
thr gln arg glu arg gln lys gly leu pro arg gln val phe glu gln asp ala ser gly  
481/161 511/171  
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA  
asp glu arg ser gly pro glu asp ser asn asp ser arg arg gly ser gly ser pro glu  
541/181 571/191  
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC  
asp thr pro arg ser ser gly ala ser ser ile phe asp leu arg asn leu ala ala asp  
601/201 631/211  
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA  
ser leu leu pro ser leu leu glu arg ala ala pro glu asp val asp arg arg asn glu  
661/221 691/231  
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG  
thr leu arg arg gln his arg pro pro ala leu leu thr leu tyr pro ala pro asp glu  
721/241 751/251  
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG  
asp glu ala val glu arg cys ser arg pro glu pro pro arg glu his phe gly gln arg  
781/261 811/271  
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC  
ile leu val lys cys leu ser leu lys phe glu ile glu ile glu pro ile phe gly ile  
841/281 871/291  
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG  
leu ala leu tyr asp val arg glu lys lys ile ser glu asn phe tyr phe asp leu  
901/301 931/311  
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC  
asn ser asp ser met lys gly leu leu arg ala his gly thr his pro ala ile ser thr  
961/321 991/331  
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC  
leu ala arg ser ala ile phe ser val thr tyr pro ser pro asp ile phe leu val ile  
1021/341 1051/351  
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG  
lys leu glu lys val leu gln gln gly asp ile ser glu cys cys glu pro tyr met val  
1081/361 1111/371

A

FIG. 6  
1 of 6

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TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC  
 leu lys glu val asp thr ala lys asn lys glu lys leu glu lys leu arg leu ala ala  
 1141/381  
 GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC  
 glu gln phe cys thr arg leu gly arg tyr arg met pro phe ala trp thr ala val his  
 1201/401  
 TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG  
 leu ala asn ile val ser ser ala gly gln leu asp arg asp ser asp ser glu gly glu  
 1261/421  
 CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG  
 arg arg pro ala trp thr asp arg arg arg arg gly pro gln asp arg ala ser ser gly  
 1321/441  
 GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT  
 asp asp ala cys ser phe ser gly phe arg pro ala thr leu thr val thr asn phe phe  
 1381/461  
 AAG GAG GAG GCT GAG CGA CTC AGT GAC GAG GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG  
 lys gln glu ala glu arg leu ser asp gly leu phe lys phe leu ala asp met arg  
 1441/481  
 CGC CGG TCC TCG CTC CTG CTG CGG CGA CTA CGT CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT  
 arg pro ser ser leu leu arg arg leu arg pro val thr ala gln leu lys ile asp ile  
 1501/501  
 TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC  
 ser pro ala pro glu asn pro his phe cys leu ser pro glu leu leu his ile lys pro  
 1561/521  
 TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC  
 tyr pro asp pro arg gly arg pro thr lys glu ile leu glu phe pro ala arg glu val  
 1621/541  
 TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC  
 tyr ala pro his thr ser tyr arg asn leu leu tyr val tyr pro his ser leu asn phe  
 1681/561  
 AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG  
 ser ser arg gln gly ser arg pro thr lys ala val arg leu phe val gln tyr met thr gly glu  
 1741/581  
 GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC  
 asp pro ser gln ala leu pro val ile phe gly lys ser ser cys ser glu phe thr arg  
 1801/601  
 GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG  
 glu ala phe thr pro val val tyr his asn lys ser pro glu phe tyr glu glu phe lys  
 1861/621  
 CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC  
 leu his leu pro ala cys val thr glu asn his his leu leu phe thr phe tyr his val  
 1921/641  
 AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA  
 ser cys gln pro arg pro gly thr ala leu glu thr pro val gly phe thr trp ile pro  
 1981/661  
 CTG CTG CAG CAC GGG CGC CTG AGG ACC GGC CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG  
 leu leu gln his gly arg leu arg thr gly pro phe cys leu pro val ser val asp gln  
 2041/681  
 CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG  
 pro pro pro ser tyr ser val leu thr pro asp val ala leu phe thr phe tyr his val  
 2101/701  
 GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG  
 asp gly his lys gly val phe ser val glu leu thr ala val ser ser val his pro gln  
 2161/721  
 GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG GTG CAC GTC CTG GAG GAG GGA GCC PTC CCA  
 asp pro tyr leu asp lys phe phe thr leu val his val leu glu glu gly ala the pro  
 2221/741  
 TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG GGC AAC GTG GAG CAG CTG CGG GCC AGT  
 phe arg leu lys asp thr val leu ser glu gly asn val glu gln glu leu arg ala ser  
 2281/761  
 CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG

leu ala ala leu arg leu ala ser pro glu pro leu val ala phe ser his his val leu  
 2341/781 2371/791  
 GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG  
 asp lys leu val arg leu val ile arg pro pro ile ile ser gly gln ile val asn leu  
 2401/801 2431/811  
 GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG  
 gly arg gly ala phe glu ala met ala his val val ser leu val his arg ser leu glu  
 2461/821 2491/831  
 GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT  
 ala ala gln asp ala arg gly his cys pro gln leu ala ala tyr val his tyr ala phe  
 2521/841 2551/851  
 CGC CTT CCT GGC ACT GAG GCC AGC CTC CCG GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT  
 arg leu pro gly thr glu pro ser leu pro asp gly ala pro pro val thr val gln ala  
 2581/861 2611/871  
 GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC  
 ala thr leu ala arg gly ser gly arg pro ala ser leu tyr leu ala arg ser lys ser  
 2641/881 2671/891  
 ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC  
 ile ser ser ser asn pro asp leu ala val ala pro gly ser val asp asp glu val ser  
 2701/901 2731/911  
 CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC  
 arg ile leu ala ser lys leu leu his glu glu leu ala leu gln trp val val ser ser  
 2761/921 2791/931  
 AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG  
 ser ala val arg glu ala ile leu gln his ala trp phe phe phe gln leu met val lys  
 2821/941 2851/951  
 AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC  
 ser met ala leu his leu leu leu gly gln arg leu asp thr pro arg lys leu arg phe  
 2881/961 2911/971  
 CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC  
 pro gly arg phe leu asp asp ile thr ala leu val gly ser val gly leu glu val ile  
 2941/981 2971/991  
 ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC  
 thr arg val his lys asp val glu leu ala glu his leu asn ala ser leu ala phe phe  
 3001/1001 3031/1011  
 CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG GGC TTT GTC TTC AGC CTG CTG CGG GCC CAC  
 leu ser asp leu leu ser leu val asp arg gly phe val phe ser leu val arg ala his  
 3061/1021 3091/1031  
 TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG  
 tyr lys gln val ala thr arg leu gln ser ser pro asn pro ala ala leu leu thr leu  
 3121/1041 3151/1051  
 CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC  
 arg met glu phe thr arg ile leu cys ser his glu his tyr val thr leu asn leu pro  
 3181/1061 3211/1071  
 TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG  
 cys cys pro leu ser pro pro ala ser pro ser pro ser val ser ser thr thr ser gln  
 3241/1081 3271/1091  
 AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT  
 ser ser thr phe ser ser gln ala pro asp pro lys val thr ser met phe glu leu ser  
 3301/1101 3331/1111  
 GGA CCA TTC CGG GAG CAC CAC TTC CTA GCT GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC  
 gly pro phe arg gln gln his phe leu ala gly leu leu thr thr glu leu ala leu ala  
 3361/1121 3391/1131  
 CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC  
 leu glu pro glu ala glu gly ala phe leu leu his lys lys ala ile ser ala val his  
 3421/1141 3451/1151  
 AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT  
 ser leu leu cys gly his asp thr asp pro arg tyr ala glu ala thr val lys ala arg  
 3481/1161 3511/1171  
 GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT  
 val ala glu leu tyr leu pro leu leu ser ile ala arg asp thr leu pro arg leu his

3541/1181

GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA  
 asp phe ala glu gly pro gly gln arg ser  
 3601/1201  
 GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC  
 glu gly glu gly asp ile ala gly thr ile  
 3661/1221  
 GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC  
 gly pro leu ala pro gly ser arg ala ser  
 3721/1241  
 GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC  
 ala gly cys ala leu ser ala glu ser ser  
 3781/1261  
 CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG  
 leu lys asn thr glu pro ala leu leu gln  
 3841/1281  
 CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT  
 leu gly arg leu leu asp leu leu tyr leu  
 3901/1301  
 AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA  
 lys ala phe glu arg ile asn ser leu thr  
 3961/1321  
 CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA  
 leu glu glu ala ile leu gly thr ile gly  
 4021/1341  
 GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC  
 glu arg ser pro phe gly asn pro glu asn  
 4081/1361  
 AAG CAA ACC TCA CAG CGC GTG GAC AAG ACC  
 lys gln thr ser asp arg val asp lys thr  
 4141/1381  
 GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA  
 glu gly asn leu ala thr glu ala ser leu  
 4201/1401  
 CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG  
 gln thr val met leu ser glu ala arg glu  
 4261/1421  
 CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC  
 leu tyr ser leu leu arg ser ala gln ser ala  
 4321/1441  
 AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG  
 arg ala leu val ser lys phe pro glu leu  
 4381/1461  
 GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT  
 asp leu cys leu arg leu leu arg his cys  
 4441/1481  
 GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA  
 ala ser ala ser leu tyr leu leu met arg  
 4501/1501  
 CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC  
 arg val lys met gln val thr met ser leu  
 4561/1521  
 AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA  
 ser glu glu his leu arg arg ser leu lys  
 4621/1541  
 GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG  
 gly leu arg asp ser thr phe ala glu gln  
 4681/1561  
 ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA  
 ile leu thr asp thr val lys met lys glu  
 4741/1581

3571/1191

AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA  
 arg leu ala ser met leu asp ser asp thr  
 3631/1211  
 AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT  
 asn pro ser val ala met ala ile ala gly  
 3691/1231  
 ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC  
 ile ser gln gly pro pro thr ala ser arg  
 3751/1251  
 CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG  
 arg thr leu leu ala cys val leu trp val  
 3811/1271  
 CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG  
 arg trp ala thr asp leu thr leu pro gln  
 3871/1291  
 TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA  
 cys leu ala ala phe glu tyr lys gly lys  
 3931/1311  
 TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG  
 phe lys lys ser leu asp met lys ala arg  
 3991/1331  
 GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT  
 ala arg gln glu met val arg arg ser arg  
 4051/1351  
 GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG  
 val arg trp arg lys ser val thr his trp  
 4111/1371  
 AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG  
 lys asp glu met glu his glu ala leu val  
 4171/1391  
 GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG  
 val val leu asp thr leu glu ile ile val  
 4231/1411  
 AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG  
 ser val leu gly ala val leu lys val val  
 4291/1431  
 CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG  
 leu phe leu gln his gly leu ala thr gln  
 4351/1451  
 CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC  
 leu phe glu glu asp thr glu leu cys ala  
 4411/1471  
 GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC  
 gly ser arg ile ser thr ile arg thr his  
 4471/1491  
 CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC  
 gln asn phe glu ile gly his asn phe ala  
 4531/1511  
 TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC  
 ser ser leu val gly thr thr gln asn phe  
 4591/1531  
 ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG  
 thr ile leu thr tyr ala glu glu asp met  
 4651/1551  
 GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG  
 val gln asp leu met phe asn leu his met  
 4711/1571  
 CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC  
 his gln glu asp pro glu met leu ile asp  
 4771/1591

CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG  
 leu met tyr arg ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu  
 4801/1601 4831/1611  
 CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG  
 gln asn met ala gly lys his ala glu leu gly asn his ala glu ala ala gln cys met  
 4861/1621 4891/1631  
 GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG  
 val his ala ala ala leu val ala glu tyr leu ala leu leu glu asp gln arg his leu  
 4921/1641 4951/1651  
 CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC  
 pro val gly cys val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile  
 4981/1661 5011/1671  
 TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG  
 ser asp asp ile leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu  
 5041/1681 5071/1691  
 CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC  
 leu gly leu val gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr  
 5101/1701 5131/1711  
 GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC  
 glu ala val asn glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr  
 5161/1721 5191/1731  
 AAG AAG CTG GCC GCG GTG CAG GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG  
 lys lys leu ala ala val his gly lys leu gln glu ala phe thr lys ile met his gln  
 5221/1741 5251/1751  
 AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC  
 ser ser gly trp glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his  
 5281/1761 5311/1771  
 TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA  
 phe gly asp leu asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala  
 5341/1781 5371/1791  
 GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG  
 glu ile ser his arg leu glu glu phe tyr thr glu arg phe gly asp val val glu  
 5401/1801 5431/1811  
 ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC  
 ile ile lys asp ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile  
 5461/1821 5491/1831  
 CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC  
 gln ile thr tyr val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr  
 5521/1841 5551/1851  
 TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG  
 phe asp arg asn tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly  
 5581/1861 5611/1871  
 CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC  
 arg ala his gly glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his  
 5641/1881 5671/1891  
 GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG  
 ala phe pro tyr ile lys thr arg ile arg val cys his arg glu glu thr val leu thr  
 5701/1901 5731/1911  
 CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC  
 pro val glu val ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr  
 5761/1921 5791/1931  
 GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC  
 glu gln asp pro pro asp ala lys met leu gln met val leu gln gly ser val gly pro  
 5821/1941 5851/1951  
 ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC  
 thr val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp.  
 5881/1961 5911/1971  
 CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA  
 pro lys leu phe arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys  
 5941/1981 5971/1991  
 TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC

cys glu asp ala leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his	
6001/2001	6031/2011
CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG	
arg glu leu glu arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln	
6061/2021	6091/2031
CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA	
arg leu pro gln leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala	
6121/2041	6151/2051
AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG	
ser phe arg lys ala asp leu OPA	
6181/2061	6211/2071
CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT	
6241/2081	6271/2091
GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA	
6301/2101	6331/2111
CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA	

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CGGTAACGCCCATTTTGTCTCCTGTAACAATTACGCGCGTGTAACGTGTAATCTTTCAAAGCCTCAGTTTATGACC  
CTGTGGAGCCAGTGAGACTTTGAAGGACTTCTG -1

1/1	ATG	ACA	CAC	CTG	AAC	AGC	CTG	GAT	GTG	CAG	CTT	GCC	CAG	GAG	CTC	GGG	GAC	TTC	ACT	GAT
Met	thr	his	leu	asn	ser	leu	asp	val	gln	leu	ala	gln	glu	leu	gly	asp	phe	thr	asp	
61/21											91/31									
GAC	GAC	TTG	GAC	GTG	GTG	TTC	ACG	CCA	AAG	GAA	TGT	AGG	ACT	TTG	CAG	CCC	TCT	TTG	CCG	
asp	asp	leu	asp	val	val	phe	thr	pro	lys	glu	cys	arg	thr	leu	gln	pro	ser	leu	pro	
121/41											151/51									
GAG	GAA	GGG	GTT	GAA	CTG	GAC	CCT	CAT	GTC	AGG	GAC	TGT	GTT	CAG	ACC	TAC	ATC	CGT	GAG	
glu	glu	gly	val	glu	leu	asp	pro	his	val	arg	asp	cys	val	gln	thr	tyr	ile	arg	glu	
181/61											211/71									
TGG	CTA	ATC	GTG	AAC	CGG	AAA	AAC	CAA	GGA	AGT	CCA	GAA	ATC	TGT	GGC	TTT	AAA	AAG	ACT	
trp	leu	ile	val	asn	arg	lys	asn	gln	gly	ser	pro	glu	ile	cys	gly	phe	lys	lys	thr	
241/81											271/91									
GGA	TCT	CGA	AAA	GAT	TTT	CAC	AAG	ACG	CTT	CCG	AAA	CAG	ACG	TTT	GAG	TCG	GAA	ACC	TTG	
gly	ser	arg	lys	asp	phe	his	lys	thr	leu	pro	lys	gln	thr	phe	glu	ser	glu	thr	leu	
301/101											331/111									
GAG	TGC	AGT	GAA	CCC	GCT	GCT	CAG	GCA	GGC	CCC	CGC	CAC	TTA	AAC	GTG	CTG	TGC	GAC	GTG	
glu	cys	ser	glu	pro	ala	ala	gln	ala	gly	pro	arg	his	leu	asn	val	leu	cys	asp	val	
361/121											391/131									
TCT	GGG	AAA	GGC	CCC	GTC	ACT	GCC	TGT	GAC	TTT	GAC	CTC	CGC	AGC	CTG	CAG	CCT	GAC	AAG	
ser	gly	lys	gly	pro	val	thr	ala	cys	asp	phe	asp	leu	arg	ser	leu	gln	pro	asp	lys	
421/141											451/151									
CGG	CTA	GAA	AAC	CTC	CTG	CAG	CAA	GTG	AGT	GCC	GAG	GAC	TTT	GAG	AAG	CAG	AAC	GAG	GAG	
arg	leu	glu	asn	leu	leu	gln	gln	val	ser	ala	glu	asp	phe	glu	lys	gln	asn	glu	glu	
481/161											511/171									
GCC	CGG	AGG	ACC	AAC	AGG	CAG	GCC	GAG	CTC	TTT	GCC	CTT	TAC	CCA	TCA	GTG	GAC	GAG	GAG	
ala	arg	arg	thr	asn	arg	gln	ala	glu	leu	phe	ala	leu	tyr	pro	ser	val	asp	glu	glu	
541/181											571/191									
GAT	GCT	GTG	GAA	ATA	CGT	CCA	GTA	CCA	GAA	TGT	CCC	AAG	GAA	CAC	CTG	GGC	AAC	AGA	ATA	
asp	ala	val	glu	ile	arg	pro	val	pro	glu	cys	pro	lys	glu	his	leu	gly	asn	arg	ile	
601/201											631/211									
TTG	GTC	AAG	TTG	CTG	ACC	TTG	AAG	TTC	GAG	ATT	GAA	ATT	GAG	CCC	CTG	TTT	GCC	AGC	ATT	
leu	val	lys	leu	leu	thr	leu	lys	phe	glu	ile	glu	ile	glu	pro	leu	phe	ala	ser	ile	
661/221											691/231									
GCC	CTC	TAC	GAT	GTT	AAA	GAA	AGG	AAA	AAG	ATC	TCA	GAA	AAT	TTT	CAC	TGT	GAC	CTG	AAC	
ala	leu	tyr	asp	val	lys	glu	arg	lys	lys	ile	ser	glu	asn	phe	his	cys	asp	leu	asn	
721/241											751/251									
TCT	GAC	CAG	TTC	AAA	GGA	TTT	CTG	CGA	GCT	CAC	ACG	CCT	TCA	GTG	GCC	GCA	TCA	AGT	CAG	
ser	asp	gln	phe	lys	gly	phe	leu	arg	ala	his	thr	pro	ser	val	ala	ala	ser	ser	gln	
781/261											811/271									
GCG	AGA	TCT	GCA	GTC	TTC	TCA	GTC	ACC	TAC	CCG	TCC	TCA	GAC	ATC	TAC	CTG	GTA	GTC	AAG	
ala	arg	ser	ala	val	phe	ser	val	thr	tyr	pro	ser	ser	asp	ile	tyr	leu	val	val	lys	
841/281											871/291									
ATT	GAA	AAA	GTC	CTG	CAG	CAG	GGA	GAT	ATT	GGA	GAC	TGT	GCA	GAG	CCC	TAC	ACG	GTT	ATC	
ile	glu	lys	val	leu	gln	gln	gly	asp	ile	gly	asp	cys	ala	glu	pro	tyr	thr	val	ile	
901/301											931/311									
AAA	GAA	AGT	GAT	GGT	GGA	AAG	AGT	AAA	GAA	AAG	ATT	GAA	AAA	CTA	AAA	CTC	CAA	GCT	GAA	
lys	glu	ser	asp	gly	gly	lys	ser	lys	glu	lys	ile	glu	lys	leu	lys	leu	gln	ala	glu	
961/321											991/331									
TCC	TTC	TGC	CAG	CGT	TTG	GGG	AAA	TAC	CGG	ATG	CCC	TTT	GCC	TGG	GCA	CCC	ATA	AGC	TTA	
ser	phe	cys	gln	arg	leu	gly	lys	tyr	arg	met	pro	phe	ala	trp	ala	pro	ile	ser	leu	



1021/341  
 TCA AGC TTC TTC AAT GTC TCC ACC CTT GAG  
 ser ser phe phe asn val ser thr leu glu  
 1081/361  
 GGG AGA AGC CCA GTG GGT GAA CGG AGG ACA TTG GCC CAA TCT AGA AGG CTT TCT GAA AGA  
 gly arg ser pro val gly glu arg thr  
 1141/381  
 GCC CTC TCC TTG GAG GAA AAT GGG GTT GGA TCC AAC TTC AAA ACC TCC ACT CTG AGC GTT  
 ala.leu ser leu glu glu asn gly val gly  
 1201/401  
 AGC AGC TTT TTC AAG CAG GAA GGA GAT CGC CTT AGC GAT GAA GAC TTA TTC AAG TTT TTA  
 ser ser phe phe lys gln glu gly asp arg  
 1261/421  
 GCT GAC TAC AAA AGA TCA TCA TCC TTA CAG AGA CGA GTC AAG TCA ATT CCA GGC TTG CTA  
 ala asp tyr lys arg ser ser leu gln arg arg val lys ser ile pro gly leu leu  
 1321/441  
 AGA CTG GAG ATT TCT ACA GCT CCA GAG ATC ATC AAT TGC TGT CTG ACT CCT GAA ATG CTG  
 arg leu glu ile ser thr ala pro glu ile  
 1381/461  
 CCC GTG AAA CCC TTT CCT GAA AAC CGG ACA CGC CGC CAC AAA GAG ATT TTG GAA TTT CCA  
 pro val lys pro phe pro glu asn arg thr  
 1441/481  
 ACA CGA GAA GTA TAT GTC CCT CAC ACT GTG TAC AGA AAC CTT CTC TAT GTC TAC CCA CAG  
 thr arg glu val tyr val pro his thr val tyr arg asn leu leu thr val tyr pro gln  
 1501/501  
 AGG CTG AAC TTT GTA AAC AAA CTA GCA TCA GCC CGG AAC ATT ACA ATA AAG ATC CAG TTT  
 arg leu asn phe val asn lys leu ala ser  
 1561/521  
 ATG TGT GGA GAA GAT GCT AGC AAT GCG ATG CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT  
 met cys gly glu asp ala ser asn ala met  
 1621/541  
 GAA TTT CTG CAG GAA GTG TAC ACA GCT GTT ACA TAC CAT AAT AAG TCT CCT GAC TTT TAT  
 glu phe leu gln glu val tyr thr ala val thr tyr his asn lys ser pro asp phe tyr  
 1681/561  
 GAA GAA GTG AAA ATT AAG CTC CCC GCT AAG CTC ACA GTA AAT CAC CAC CTC CTG TTC ACC  
 glu glu val lys ile lys leu pro ala lys leu thr val asn his his leu leu phe thr  
 1741/581  
 TTC TAC CAT ATC AGC TGT CAG CAG AAG CAA GGA GCC TCC GTG GAA ACT CTC CTG GGA TAT  
 phe tyr his ile ser cys gln gln lys gln  
 1801/601  
 TCA TGG CTG CCA ATT CTC TTA AAT GAA CGT CTT CAA ACT GGA TCC TAC TGT CTC CCA GTT  
 ser trp leu pro ile leu leu asn glu arg  
 1861/621  
 GCC TTG GAA AAA TTG CCA CCC AAC TAC TCC ATG CAT TCT GCT GAG AAA GTC CCA TTA CAG  
 ala leu glu lys leu pro pro asn tyr ser met his ser ala glu lys val pro leu gln  
 1921/641  
 AAT CCT CCC ATT AAG TGG GCT GAA GGA CAT AAG GGA GTA TTT AAT ATT GAA GTG CAA GCT  
 asn pro pro ile lys trp ala glu gly his lys gly val phe asn ile glu val gln ala  
 1981/661  
 GTT TCT TCT GTA CAC ACC CAG GAC AAC CAC CTG GAG AAG TTC TTC ACC CTC TGC CAC TCC  
 val ser ser val his thr gln asp asn his leu glu lys phe phe thr leu cys his ser  
 2041/681  
 CTG GAG AGC CAG GTG ACC TTC CCC ATC CGC GTG CTG GAT CAG AAA ATC AGC GAG ATG GCG  
 leu glu ser gln val thr phe pro ile arg val leu asp gln lys ile ser glu met ala  
 2101/701  
 CTG GAG CAT GAG CTG AAG CTC AGC ATC ATC TGC CTG AAC TCC TCC GCG CTG GAG CCG CTC  
 leu glu his glu leu lys leu ser ile ile cys leu asn ser ser arg leu glu pro leu

2161/721	GTG CTC TTC CTG CAC CTG GTG CTG GAC AAG	2191/731	CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC
val leu phe leu his leu val leu asp lys	leu phe gln leu ser val gln pro met val		
2221/741	ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG	2251/751	TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC
ile ala gly gln thr ala asn phe ser gln	phe ala phe glu ser val val ala ile ala		
2281/761	AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC	2311/771	AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG
asn ser leu his asn ser lys asp leu ser	lys asp gln his gly arg asn cys leu leu		
2341/781	GCT TCC TAC GTG CAC TAC GTC TTC CGC CTG	2371/791	CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA
ala ser tyr val his tyr val phe arg leu	pro glu val gln arg asp val pro lys ser		
2401/801	GGC GCT CCC ACT GCC CTC CTA GAC CCT CGG	2431/811	AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT
gly ala pro thr ala leu leu asp pro arg	ser tyr his thr tyr gly arg thr ser ala		
2461/821	GCT GCT GTG AGT TCA AAG CTG CTG CAG GCC	2491/831	CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC
ala ala val ser ser lys leu leu gln ala	arg val met ser ser ser asn pro asp leu		
2521/841	GCG GGG ACA CAC TCC GCA GCA GAC GAG GAA	2551/851	GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC
ala gly thr his ser ala ala asp glu glu	val lys asn ile met ser ser lys ile ala		
2581/861	GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT	2611/871	TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA
asp arg asn cys ser arg met ser tyr tyr	cys ser gly ser ser asp ala pro ser ser		
2641/881	CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG	2671/891	CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG
pro ala ala pro arg pro ala ser lys lys	his phe his glu glu leu ala leu gln met		
2701/901	GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG	2731/911	GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG
val val ser thr gly met val lys ser met	ala gln his val his asn met asp lys arg		
2761/921	GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC	2791/931	CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT
asp ser phe arg arg thr arg phe ser asp	arg phe met asp asp ile thr ile val		
2821/941	AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT	2851/951	TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG
asn val val thr ser glu ile ala ala leu	leu val lys pro gln lys glu asn glu gln		
2881/961	GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC	2911/971	TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT
ala glu lys met asn ile ser leu ala phe	phe leu tyr asp leu leu ser leu met asp		
2941/981	CGG GGC TTT GTG TTT AAC CTC ATC AGA CAT	2971/991	TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT
arg gly phe val phe asn leu ile arg his	tyr cys ser gln leu ser ala lys leu ser		
3001/1001	AAC CTT CCA ACG CTC ATT TCC ATG AGG CTA	3031/1011	GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG
asn leu pro thr leu ile ser met arg leu	glu phe leu arg ile leu cys ser his glu		
3061/1021	CAT TAC CTC AAT CTG AAC CTT TTT TTT ATG	3091/1031	AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT
his tyr leu asn leu asn leu phe phe met	asn ala asp thr ala pro thr ser pro cys		
3121/1041	CCT TCC ATA TCT TCC CAG AAC TCA AGC TCC	3151/1051	TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC
pro ser ile ser ser gln asn ser ser ser	cys ser ser phe gln asp gln lys ile ala		
3181/1061	AGC ATG TTC GAT CTG ACT TCC GAG TAC CGC	3211/1071	CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC
ser met phe asp leu thr ser glu tyr arg	gln gln his phe leu thr gly leu leu phe		
3241/1081	ACA GAA CTG GCT GCT GCC CTG GAT GCC GAA	3271/1091	GGG GAA GGA ATC AGC AAA GTA CAA AGG AAA
thr glu leu ala ala ala leu asp ala glu	gly glu gly ile ser lys val gln arg lys		

3301/1101 GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA  
 ala val ser ala ile his ser leu leu ser ser his asp leu asp pro arg cys val lys  
 3361/1121 CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT  
 pro glu val lys val lys ile ala ala leu tyr leu pro leu val gly ile ile leu asp  
 3421/1141 GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC  
 ala leu pro gln leu cys asp phe thr val ala asp thr arg arg tyr arg thr ser gly  
 3481/1161 TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA  
 ser asp glu glu gln glu gly ala gly ala ile asn gln asn val ala leu ala ile ala  
 3541/1181 GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG  
 gly asn asn phe asn leu lys thr ser gly ile val leu ser ser leu pro tyr lys gln  
 3601/1201 TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG  
 tyr asn met leu asn ala asp thr thr arg asn leu met ile cys phe leu trp ile met  
 3661/1221 AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC  
 lys asn ala asp gln ser leu ile arg lys trp ile ala asp leu pro ser thr gln leu  
 3721/1241 AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG  
 asn arg ile leu asp leu leu phe ile cys val leu cys phe glu tyr lys gly lys gln  
 3781/1261 AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG  
 ser ser asp lys val ser thr gln val leu gln lys ser arg asp val lys ala arg leu  
 3841/1281 GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA  
 glu glu ala leu leu arg gly glu gly ala arg gly glu met met arg arg arg ala pro  
 3901/1301 GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT  
 gly asn asp arg phe pro gly leu asn glu asn leu arg trp lys lys glu gln thr his  
 3961/1321 TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG  
 trp arg gln ala asn glu lys leu asp lys thr lys ala glu leu asp gln glu ala leu  
 4021/1341 ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT  
 ile ser gly asn leu ala thr glu ala his leu ile ile leu asp met gln glu asn ile  
 4081/1361 ATC CAG GCG AGC TCG GCT GTC GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG  
 ile gln ala ser ser ala leu asp cys lys asp ser leu leu gly gly val leu arg val  
 4141/1381 CTG GTG AAT TCT CTG AAC TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA  
 leu val asn ser leu asn cys asp gln ser thr thr tyr leu thr his cys phe ala thr  
 4201/1401 CTC CGT GCT CTC ATC GCC AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT  
 leu arg ala leu ile ala lys phe gly asp leu leu phe glu glu val glu gln cys  
 4261/1421 TTC CAG CTA TGT CAC CAA GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC  
 phe asp leu cys his gln val leu his his cys ser ser ser met asp val thr arg ser  
 4321/1441 CAA GCC TGT GCC ACC CTT TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT  
 gln ala cys ala thr leu tyr leu leu met arg phe ser phe gly ala thr ser asn phe  
 4381/1461 GCA AGA GTA AAG ATG CAA GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC  
 ala arg val lys met gln val thr met ser leu ala ser leu val gly arg ala pro asp

4441/1481  
TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC  
phe asn glu glu his leu arg arg ser leu arg thr ile leu ala tyr ser glu glu asp  
4501/1501  
ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT  
thr ala met gln met thr pro phe pro thr gln val glu glu leu leu cys asn leu asn  
4561/1521  
AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG  
ser ile leu tyr asp thr val lys met arg glu phe gln glu asp pro glu met leu met  
4621/1541  
GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG  
asp leu met tyr arg ile ala lys ser tyr gln ala ser pro asp leu arg leu thr trp  
4681/1561  
CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC  
leu gln asn met ala glu lys his thr lys lys lys cys tyr thr glu ala ala met cys  
4741/1581  
CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC  
leu val his ala ala ala leu val ala glu tyr leu ser met leu glu asp his ser tyr  
4801/1601  
CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG  
leu pro val gly ser val ser phe gln asn ile ser ser asn val leu glu glu ser val  
4861/1621  
GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC  
val ser glu asp thr leu ser pro asp glu asp gly val cys ala gly gln tyr phe thr  
4921/1641  
GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA  
glu ser gly leu val gly leu leu glu gln ala ala glu leu phe ser thr gly gly leu  
4981/1661  
TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA  
tyr glu thr val asn glu val tyr lys leu val ile pro ile leu glu ala his arg glu  
5041/1681  
TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC  
phe arg lys leu thr leu thr his ser lys leu gln arg ala phe asp ser ile val asn  
5101/1701  
AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT  
lys asp his lys arg met phe gly thr tyr phe arg val gly phe phe gly ser lys phe  
5161/1721  
GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG  
gly asp leu asp glu gln glu phe val tyr lys glu pro ala ile thr lys leu pro glu  
5221/1741  
ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG  
ile ser his arg leu glu ala phe tyr gly gln cys phe gly ala glu phe val glu val  
5281/1761  
ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG  
ile lys asp ser thr pro val asp lys thr lys leu asp pro asn lys ala tyr ile gln  
5341/1781  
ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT  
ile thr phe val glu pro tyr phe asp glu tyr glu met lys asp arg val thr tyr phe  
5401/1801  
GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG  
glu lys asn phe asn leu arg arg phe met tyr thr thr pro phe thr leu glu gly arg  
5461/1821  
CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC  
pro arg gly glu leu his glu gln tyr arg arg asn thr val leu thr thr met his ala  
5521/1841  
TTC CCC TAC ATC AAG ACC AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG  
phe pro tyr ile lys thr arg ile ser val ile gln lys glu glu phe val leu thr pro

5581/1861  
ATT GAA GTT GCC ATT GAA GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC  
ile glu val ala ile glu asp met lys lys lys thr leu gln leu ala val ala ile asn  
5641/1881  
CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT  
gln glu pro pro asp ala lys met leu gln met val leu gln gly ser val gly ala thr  
5701/1901  
GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA  
val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro ala asp pro  
5761/1921  
AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT  
lys leu tyr arg his his asn lys leu arg leu cys phe lys glu phe ile met arg cys  
5821/1941  
GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG  
gly glu ala val glu lys asn lys arg leu ile thr ala asp gln arg glu tyr gln gln  
5881/1961  
GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA  
glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys  
5941/1981  
ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC  
ile pro glu leu tyr lys pro ile phe arg val glu ser gln lys arg ser phe his  
6001/2001  
AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC TAA  
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

GAAAAAGCCATCTTCATCTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAATGGGACATT  
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAAATTATT  
CCCAAAATGGACTCTGACCAGATTTTGGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT  
TTATTAAGGTGTGTTTTCCACAATGTACCAAAACAGGCATAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATC  
TGAGAGATGATTTCCCTCTGGCCATATTGAATTTATTGGAGTAACCTCAAATTTGCTGAGGAAAAATGGAAAAATTATCC  
ACCACTCGATTCAAACCTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACTTTGAGGAGTACGAAACATTTTCAATAAT  
CTACAAGGGGAAGCCTTACTACAATTTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATTATTTGTGAATTTGTTAC  
CCTTTTGGTAAATGGTGGGACTAATGCTGTATAGTTATTTTGTGTTTATTATTACTGTTACATTAATTTACATGCTATTA  
TAGAAGAATACATTTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT  
CACTTAAATGGAAACAATTTCTCCGATAATGCTTTGCTTTTTTCTTATGTCACTCTTGCTACTACTATTTTCTCTCTC  
TCTGGGACCAAGTTCTTTTTATAAGCAATAATATCTCTGTTTTCATTTCAGAACATTTGCTGTCTGTCAGCATATGT  
ATATCAGCTACAAAATATATTTCACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTTTGG  
AGAATTAATATATATTTTAAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAAA  
AAAAAAAAAAAACTCG

Exon 1A' (-216 to -95, 'P2')  
 CCCATTAGGAGGTCTACCCACCCCTGATTGGAGGACATGGGGCTGGAGGCTGAAGATGGAGACCAGATCACAAGGGATCTAATAAG  
 CTTTGCTGAACAGTTTGAAGCTTTATTCTACAGACTCT -95

Exon 1B (-381 to -95, 'GR3.3')  
 AAATTTTAGTTGGAGAATGCACAGGAGAAGGTGTAGACATAGTTTTGTCTGTGTGCAGACACCTTGATAGCAAACTATAGGTAG  
 AGGCTTCTGGAGGCAGGATTGCTCTTAGTCTAAGGCTTTATGGTAACATTTGCAGGGGATACGGGTAGCATTACAAAATGGGGA  
 TGCTTCAGGAAGGGCGTGGCGAGTGCTTCTTGCTATTACTTCTGTAAACCAAGCTAGCTAGGCTTTTGGGTATGTTCAACAC  
 TGCATGGCCTTTGGAGCACTTTTATGGGAAGA -95

Exon 1C' (-415 to -95, 'GR3.4')  
 AAAGACAGGAACGCCTGCCACATTGAGAGGATAGCATTTTAGTTGGAGAGTGTACAGGAGAAGGTGTAGACATAGTTTTGTCTG  
 TGTGCAGACACCTNGATAGCAAACTATAGGTAGAGGCTTCTGGAGGCAGGATTGCTCTTAGTCTAAGGTCTTATGGTAACATTT  
 GCAGGGGATACGGGTTAGCATTACAAAATGGGGATGCTTCAGGAAGGGCGTGGGCGAGTGCTTCTTGCTATTACTTCTTGTAACC  
 AAAGCTAGTCTAGGCTTTTGGGTATGTTCAACACTGCATGGCCTTTGGAGCACTTTTATGGGAAGA -95

Exon 1D (-186 to -95, 'GR8.2')  
 AATTAGAAACAACGGGGTTCTGCGACAGAGTGGGCGCAGGGTCATCCACCGCAGGGAGAGTGTGTCCTCGGGGACACGCGAGCG  
 CTCAGA -95

Exon 1E (-217 to -95, 'GR8.3')  
 AAGTTGAAGGGGTGCTGCTGCGGAGGAAGGGCATTAGAAACAACGGGGTCTGCGCAGAGTGGGCGCAGGGTCATCCACCGCAG  
 GGAGAGTGTGTCCTCGGGGACACGCGAGCGCTCCAGA -95

Exon 1F (-166 to -95, 'GR8.4')  
 AAACCAAAGCTAGTCTAGGCTTCTGGGTATGTTCAACACTGCATGGCCTTTGGAGCACTTATATGGGAAGA -95

Exon 1G (-250 to -95, EST 850011)  
 GTCCACCCGCCCGCAGGTCGCCGCCGCCGCCGAGACCCGCCGCCGCCGCTGCCATGGCCGAAGTGCGCCAATTACCAAACG  
 GTCAGCAAGCCTGGCAGCGCGCTGANATCCGGCAGACGTGTCTGAGGCCGTGCGGGGCTCCGTGGTGCT -95

Exon 1H (-187 to -95, 'GR1988')  
 AAATTAGAAACAACGGGGTTCTGCGCAGAGTGGGCGCAGGGTCATCCACCGCAGGGAGAGTGTGTCCTCGGGGACACGCGAGC  
 GCTCAGA -95

Exon 1I (-144 to -95, 'GR2005')  
 AACTCCCGGATGCGGCTGCACAGCAACATCAGTGCAGGGAGCCCCAGC -95

Exon 1J (-131 to -95, 'GR1986')  
 AACCCAGAAAGCCCCGGCGCCCAAGCTCGGGCTGGC -95

-94

G GAA AAG GCC AAA GTT GTT GAG CCC CTG GAC TAT GAG AAT GTT ATT GCC CAA AGA AAA -37

ACC CAG ATT TAC AGC GAC CCC CTC CGA GAT CTG CTT 1 ATG TTC CCA ATG GAA GAT ATA TCT 24  
 met phe pro met glu asp ile ser

ATC TCG GTG ATA GGT CGT CAG CGC AGA ACG GTG CAG TCT ACT GTA CCA GAA GAT GCT GAA 84  
 ile ser val ile gly arg gln arg arg thr val gln ser thr val pro glu asp ala glu

AAG AGG GCC CAG AGT TTA TTT GTT AAA GAG TGT ATT AAA ACC TAT AGC ACA GAT TGG CAC 144  
 lys arg ala gln ser leu phe val lys glu cys ile lys thr tyr ser thr asp trp his.

GTG GTA AAC TAC AAG TAT GAG GAC TTC TCT GGG GAC TTT CGA ATG TTG CCA TGT AAA TCT 204  
val val asn tyr lys tyr glu asp phe ser gly asp phe arg met leu pro cys lys ser

TTG AGA CCA GAA AAG ATT CCT AAT CAT GTA TTT GAG ATA GAT GAA GAC TGT GAG AAA GAT 264  
leu arg pro glu lys ile pro asn his val phe glu ile asp glu asp cys glu lys asp

GAG GAC TCA TCT TCT TTA TGT TCT CAG AAG GGT GGT GTG ATA AAA CAA GGC TGG TTG CAT 324  
glu asp ser ser ser leu cys ser gln lys gly gly val ile lys gln gly trp leu his

AAA GCA AAT GTA AAT AGT ACC ATC ACA GTA ACC ATG AAG GTA TTC AAG AGA CGA TAT TTT 384  
lys ala asn val asn ser thr ile thr val thr met lys val phe lys arg arg tyr phe

TAC TTG ACC CAA CTT CCT GAC GGT TCA TAT ATT CTC AAT TCC TAT AAA GAT GAG AAA AAT 444  
tyr leu thr gln leu pro asp gly ser tyr ile leu asn ser tyr lys asp glu lys asn

TCA AAA GAA TCG AAA GGT TGC ATC TAC TTG GAC GCC TGC ATT GAT GTT GTT CAG TGC CCC 504  
ser lys glu ser lys gly cys ile tyr leu asp ala cys ile asp val val gln cys pro

AAA ATG CGC CGT CAT GCT TTT GAA CTC AAG ATG TTA GAT AAA TAT AGC CAT TAT CTG GCT 564  
lys met arg arg his ala phe glu leu lys met leu asp lys tyr ser his tyr leu ala

GCT GAA ACT GAG CAG GAA ATG GAG GAA TGG TTG ATA ACT TTG AAA AAG ATT ATT CAG ATC 624  
ala glu thr glu gln glu met glu glu trp leu ile thr leu lys lys ile ile gln ile

AAC ACC GAC AGT TTA GTT CAA GAA AAA AAG GAG ACG GTA GAA ACA GCA CAA GAT GAT GAA 684  
asn thr asp ser leu val gln glu lys lys glu thr val glu thr ala gln asp asp glu

ACT AGC AGC CAA GGA AAA GCC GAG AAC ATC ATG GCA AGT TTG GAA AGG AGC ATG CAT CCG 744  
thr ser ser gln gly lys ala glu asn ile met ala ser leu glu arg ser met his pro

GAA CTG ATG AAG TAT GGA AGA GAA ACT GAA CAA CTA AAC AAA CTC AGT AGA GGA GAT GGA 804  
glu leu met lys tyr gly arg glu thr glu gln leu asn lys leu ser arg gly asp gly

AGA CAG AAT CTC TTT TCT TTT GAT TCA GAA GTT CAG AGG TTG GAC TTT TCA GGA ATT GAA 864  
arg gln asn leu phe ser phe asp ser glu val gln arg leu asp phe ser gly ile glu

CCT GAT ATA AAG CCA TTT GAA GAA AAA TGC AAT AAA CGT TTC CTG GTG AAT TGC CAT GAT 924  
pro asp ile lys pro phe glu glu lys cys asn lys arg phe leu val asn cys his asp

TTA ACT TTC AAT ATC TTG GGC CAA ATT GGA GAC AAT GCA AAA GGA CCA CCC ACA AAT GTT 984  
leu thr phe asn ile leu gly gln ile gly asp asn ala lys gly pro pro thr asn val

GAG CCC TTT TTT ATC AAT CTT GCC TTA TTT GAT GTA AAG AAC AAT TGT AAG ATT TCA GCA 1044  
glu pro phe phe ile asn leu ala leu phe asp val lys asn asn cys lys ile ser ala

GAC TTT CAT GTA GAC CTG AAT CCC CCA TCT GTC CGT GAA ATG CTG TGG GGC TCT TCA ACC 1104  
asp phe his val asp leu asn pro pro ser val arg glu met leu trp gly ser ser thr

CAA CTG GCC AGT GAC GGT AGC CCA AAG GGC TCT TCA CCC GAA TCT TAC ATT CAT GGA ATT 1164  
gln leu ala ser asp gly ser pro lys gly ser ser pro glu ser tyr ile his gly ile

GCC GAA TCT CAG TTA CGC TAC ATA CAA CAG GGA ATT TTC TCA GTG ACG AAT CCA CAT CCT 1224  
ala glu ser gln leu arg tyr ile gln gln gly ile phe ser val thr asn pro his pro

GAA ATT TTT CTA GTT GCC AGA ATT GAA AAG GTA CTA CAG GGA AAC ATT ACA CAC TGT GCA 1284  
glu ile phe leu val ala arg ile glu lys val leu gln gly asn ile thr his cys ala

GAA CCC TAT ATC AAA AAT TCT GAT CCA GTA AAG ACG GCC CAG AAG GTG CAC AGG ACA GCT 1344  
 glu pro tyr ile lys asn ser asp pro val lys thr ala gln lys val his arg thr ala  
 AAA CAA GTG TGT AGC CGC CTT GGA CAA TAC AGA ATG CCC TTC GCT TGG GCT GCC AGA CCC 1404  
 lys gln val cys ser arg leu gly gln tyr arg met pro phe ala trp ala ala arg pro  
 ATT TTC AAA GAT ACT CAA GGC TCT CTT GAT CTG GAT GGG AGA TTT TCT CCT CTG TAT AAA 1464  
 ile phe lys asp thr gln gly ser leu asp leu asp gly arg phe ser pro leu tyr lys  
 CAA GAC AGT AGC AAG CTT TCA AGT GAA GAC ATT CTC AAG TTG CTC TCA GAA TAT AAG AAG 1524  
 gln asp ser ser lys leu ser ser glu asp ile leu lys leu leu ser glu tyr lys lys  
 CCA GAA AAG ACC AAA CTG CAG ATT ATT CCT GGG CAG CTA AAC ATC ACA GTA GAA TGT GTT 1584  
 pro glu lys thr lys leu gln ile ile pro gly gln leu asn ile thr val glu cys val  
 CCT GTG GAT TTA TCA AAT TGT ATT ACT TCT TCA TAT GTG CCC TTG AAG CCT TTT GAA AAG 1644  
 pro val asp leu ser asn cys ile thr ser ser tyr val pro leu lys pro phe glu lys  
 AAT TGC CAA AAT ATT ACT GTG GAG GTT GAA GAG TTT GTT CCA GAA ATG ACA AAA TAT TGT 1704  
 asn cys gln asn ile thr val glu val glu glu phe val pro glu met thr lys tyr cys  
 TAT CCA TTT ACT ATT TAC AAA AAC CAT CTG TAT GTA TAT CCC CTG CAA TTA AAA TAC GAT 1764  
 tyr pro phe thr ile tyr lys asn his leu tyr val tyr pro leu gln leu lys tyr asp  
 AGC CAG AAA ACA TTT GCC AAG GCA AGG AAC ATT GCA GTC TGT GTG GAA TTC CGG GAT TCA 1824  
 ser gln lys thr phe ala lys ala arg asn ile ala val cys val glu phe arg asp ser  
 GAT GAA AGT GAC GCT AGT GCC CTA AAG TGT ATT TAT GGA AAA CCT GCA GGG TCT GTT TTT 1884  
 asp glu ser asp ala ser ala leu lys cys ile tyr gly lys pro ala gly ser val phe  
 ACC ACA AAT GCT TAT GCT GTT GTC TCG CAT CAC AAC CAA AAT CCA GAG TTC TAT GAT GAG 1944  
 thr thr asn ala tyr ala val val ser his his asn gln asn pro glu phe tyr asp glu  
 ATT AAA ATT GAG CTT CCC ATT CAC CTA CAT CAA AAA CAT CAT TTG CTT TTC ACT TTT TAT 2004  
 ile lys ile glu leu pro ile his leu his gln lys his his leu leu phe thr phe tyr  
 CAT GTA AGT TGT GAA ATT AAC ACA AAG GGA ACA ACC AAA AAG CAA GAC ACA GTT GAA ACT 2064  
 his val ser cys glu ile asn thr lys gly thr thr lys lys gln asp thr val glu thr  
 CCA GTT GGG TTT GCC TGG GTA CCT TTG CTG AAA GAT GGT AGA ATC ATC ACA TTT GAG CAG 2124  
 pro val gly phe ala trp val pro leu leu lys asp gly arg ile ile thr phe glu gln  
 CAG CTG CCA GTT TCC GCC AAT CTT CCC CCA GGC TAC TTG AAT CTG AAT GAT GCA GAA TCA 2184  
 gln leu pro val ser ala asn leu pro pro gly tyr leu asn leu asn asp ala glu ser  
 AGA AGG CAA TGT AAC GTG GAT ATT AAA TGG GTA GAT GGT GCA AAG CCT TTG TTG AAG TTT 2244  
 arg arg gln cys asn val asp ile lys trp val asp gly ala lys pro leu leu lys phe  
 AAA AGC CAC TTA GAA TCT ACC ATT TAC ACT CAA GAT CTG CAT GTG CAC AAA TTC TTC CAT 2304  
 lys ser his leu glu ser thr ile tyr thr gln asp leu his val his lys phe phe his  
 CAT TGC CAG CTG ATT CAG TCA GGC TCG AAA GAA GTT CCA GGG GAG CTC ATT AAA TAT TTA 2364  
 his cys gln leu ile gln ser gly ser lys glu val pro gly glu leu ile lys tyr leu  
 AAG TGT TTG CAT GCC ATG GAG ATC CAA GTC ATG ATA CAG TTT CTA CCT GTA ATT CTT ATG 2424  
 lys cys leu his ala met glu ile gln val met ile gln phe leu pro val ile leu met  
 CAA CTC TTC CGA GTT CTC ACA AAT ATG ACC CAT GAA GAT GAC GTT CCT ATC AAC TGC ACC 2484  
 gln leu phe arg val leu thr asn met thr his glu asp asp val pro ile asn cys thr



ATG GTT CTC TTA CAT ATT GTA TCA AAG TGC CAT GAA GAA GGC TTG GAT AGT TAT CTA AGA 2544  
 met val leu leu his ile val ser lys cys his glu glu gly leu asp ser tyr leu arg  
 TCA TTC ATA AAG TAT AGC TTC CGA CCT GAA AAA CCG AGT GCT CCT CAG GCC CAG CTG ATA 2604  
 ser phe ile lys tyr ser phe arg pro glu lys pro s r ala pro gln ala gln leu ile  
 CAT GAA ACC CTG GCT ACT ACG ATG ATA GCA ATA TTG AAA CAG TCT GCA GAT TTT TTA TCA 2664  
 his glu thr leu ala thr thr met ile ala ile leu lys gln ser ala asp phe leu ser  
 ATA AAC AAA TTG CTA AAG TAC TCA TGG TTT TTC TTT GAA ATA ATT GCA AAG TCA ATG GCC 2724  
 ile asn lys leu leu lys tyr ser trp phe phe phe glu ile phe ala lys ser met ala  
 ACA TAC TTG TTG GAA GAG AAT AAG ATT AAG CTT CCC CGA GGC CAG AGA TTT CCC GAG ACA 2784  
 thr tyr leu leu glu glu asn lys ile lys leu pro arg gly gln arg phe pro glu thr  
 TAT CAT CAT GTC TTA CAT TCA CTG CTT CTT GCA ATA ATT CCC CAT GTG ACT ATT CGG TAT 2844  
 tyr his his val leu his ser leu leu leu ala ile ile pro his val thr ile arg tyr  
 GCG GAG ATT CCC GAT GAG TCC AGA AAT GTG AAC TAT AGT TTG GCT AGC TTC CTG AAG CGC 2904  
 ala glu ile pro asp glu ser arg asn val asn tyr ser leu ala ser phe leu lys arg  
 TGT TTG ACA CTA ATG GAT AGA GGA TTT ATT TTC AAT TTA ATA AAT GAC TAT ATA TCT GGA 2964  
 cys leu thr leu met asp arg gly phe phe phe asn leu ile asn asp tyr ile ser gly  
 TTC AGC CCC AAA GAT CCT AAG GTT CTG GCT GAA TAC AAG TTT GAA TTT CTG CAA ACA ATT 3024  
 phe ser pro lys asp pro lys val leu ala glu tyr lys phe glu phe leu gln thr ile  
 TGC AAT CAC GAA CAT TAC ATT CCT CTG AAC TTG CCA ATG GCA TTT GCA AAA CCT AAA CTG 3084  
 cys asn his glu his tyr ile pro leu asn leu pro met ala phe ala lys pro lys leu  
 CAG CGG GTT CAA GAT TCA AAT CTT GAA TAC AGT TTA TCA GAT GAG TAT TGC AAG CAT CAC 3144  
 gln arg val gln asp ser. asn leu glu tyr ser leu ser asp glu tyr cys lys his his  
 TTC TTG GTT GGT CTA CTT CTG AGG GAA ACT TCC ATT GCT CTT CAG GAC AAT TAT GAG ATC 3204  
 phe leu val gly leu leu leu arg glu thr ser ile ala leu gln asp asn tyr glu ile  
 AGA TAT ACA GCT ATC TCT GTT ATA AAG AAT CTT TTG ATA AAA CAT GCA TTT GAC ACA AGA 3264  
 arg tyr thr ala ile ser val ile lys asn leu leu ile lys his ala phe asp thr arg  
 TAC CAG CAC AAG AAC CAA CAA GCC AAA ATA GCA CAA TTG TAC CTC CCC TTT GTT GGA CTA 3324  
 tyr gln his lys asn gln gln ala lys ile ala gln leu tyr leu pro phe val gly leu  
 CTT TTG GAA AAT ATA CAG CGA TTA GCA GGT CGA GAT ACC TTG TAT TCT TGT GCA GCC ATG 3384  
 leu leu glu asn ile gln arg leu ala gly arg asp thr leu tyr ser cys ala ala met  
 CCT AAT TCT GCA TCC AGA GAT GAG TTT CCA TGT GGC TTT ACT TCA CCT GCC AAT AGA GGG 3444  
 pro asn ser ala ser arg asp glu phe pro cys gly phe thr ser pro ala asn arg gly  
 AGT CTG AGC ACT GAC AAA GAC ACC GCT TAT GGG TCT TTT CAA AAT GGA CAT GGA ATT AAG 3504  
 ser leu ser thr asp lys asp thr ala tyr gly ser phe gln his gly ile lys  
 AGA GAA GAT TCA AGA GGT TCC CTC ATC CCA GAA GGA GCA ACA GGA TTT CCA CAT CAG GCC 3564  
 arg glu asp ser arg gly ser leu ile pro glu gly ala thr gly phe pro asp gln gly  
 AAC ACT GGT GAA AAT ACC CGA CAG AGT TCT ACA AGG AGT AGT GTA TCC CAG TAT AAC CGC 3624  
 asn thr gly glu asn thr arg gln ser ser thr arg ser ser val ser gln tyr asn arg

CTG GAT CAG TAT GAA ATC AGA AGC CTC CTG ATG TGC TAC CTG TAT ATA GTA AAA ATG ATT 3684  
leu asp gln tyr glu ile arg ser leu leu met cys tyr leu tyr ile val lys met ile

TCA GAA GAT ACT CTC TTA ACT TAC TGG AAT AAA GTA TCA CCT CAG GAG CTC ATA AAC ATT 3744  
ser glu asp thr leu leu thr tyr trp asn lys val ser pro gln glu leu ile asn ile

CTT ATA CTT TTA GAA GTA TGC TTG TTT CAC TTT AGA TAT ATG GGG AAA AGA AAC ATA GCA 3804  
leu ile leu leu glu val cys leu phe his phe arg met gly lys arg asn ile ala

AGG GTG CAT GAT GCC TGG TGC TCA AAA CAC TTC GGA ATA GAC CGA AAA TCG CAA ACC ATG 3864  
arg val his asp ala trp leu ser lys his phe gly ile asp arg lys ser gln thr met

CCT GCT CTT CGA AAC AGA TCA GGA GTA ATG CAG GCC CGG CTT CAG CAT CTT AGT AGC CTA 3924  
pro ala leu arg asn arg ser gly val met gln ala arg leu gln his leu ser ser leu

GAA AGT TCA TTT ACA CTT AAT CAC AGT TCT ACA ACA ACT GAA GCA GAC ATT TTC CAC GAG 3984  
glu ser ser phe thr leu asn his ser ser thr thr glu ala asp ile phe his gln

GCA CTT CTT GAA GGC AAT ACA GCT ACT GAA GTT TCC CTA ACA GTA CTA GAC ACC ATA TCA 4044  
ala leu leu glu gly asn thr ala thr glu val ser leu thr val leu asp thr ile ser

TTT TTC ACT CAG TGC TTC AAG ACC CAA CTT TTA AAT AAT GAT GGC CAT AAC CCA TTA ATG 4104  
phe phe thr gln cys phe lys thr gln leu leu asn asn asp gly his asn pro leu met

AAA AAA GTG TTT GAT ATA CAT CTT GCT TTT CTT AAA AAT GGA CAA TCT GAA GTG TCG CTG 4164  
lys lys val phe asp ile his leu ala phe leu lys asn gly gln ser glu val ser leu

AAA CAT GTA TTT GCC TCA CTG AGA GCT TTC ATC AGT AAG TTT CCT TCA GCA TTT TTC AAA 4224  
lys his val phe ala ser leu arg ala phe ile ser lys phe pro ser ala phe phe lys

GGA AGA GTA AAC ATG TGT GCT GCA TTT TGC TAT GAG GTT TTA AAG TGC TGC ACA TCG AAG 4284  
gly arg val asn met cys ala ala phe cys tyr glu val leu lys cys cys thr ser lys

ATT AGC TCA ACC AGG AAT GAA GCA TCT GCA CTT TTG TAT CTT TTG ATG AGA AAC AAC TTT 4344  
ile ser ser thr arg asn glu ala ser ala leu leu tyr leu leu met arg asn asn phe

GAG TAT ACC AAA AGG AAA ACC TTT TTG AGG ACA CAT CTA CAG ATA ATA ATT GCT GTA AGC 4404  
glu tyr thr lys arg thr lys thr phe leu arg thr his leu gln ile ile ile ala val ser

CAA CTG ATA GCT GAT GTA GCA CTA AGC GGA GGA TCA AGA TTT CAG GAG TCT TTA TTC ATT 4464  
gln leu ile ala asp val ala leu phe ser gly gly ser arg phe gln glu ser leu phe ile

ATC AAT AAT TTT GCA AAT AGT GAC AGA CCT ATG AAG GCA ACT GCC TTT CCC GCA GAA GTC 4524  
ile asn asn phe ala asn ser asp arg pro met lys ala thr ala phe pro ala glu val

AAA GAC TTG ACC AAG AGA ATC CGC ACT GTT CTT ATG GCC ACT GCC CAA ATG AAG GAG CAT 4584  
lys asp leu thr lys arg ile arg thr val leu met ala thr ala gln met lys glu his

GAG AAA GAC CCT GAA ATG CTA ATT GAT CTC CAG TAT AGC TTA GCC AAG TCC TAT GCA AGC 4644  
glu lys asp pro glu met leu ile asp leu gln tyr ser leu ala lys ser tyr ala ser

ACC CCA GAG CTC AGG AAA ACC TGG CTT GAT AGC ATG GCC AAG ATT CAT GTA AAA AAT GGA 4704  
thr pro glu leu arg lys thr trp leu asp ser met ala lys ile his val lys asn gly

GAT TTT TCA GAG GCT GCG ATG TGT TAT GTC CAT GTA GCA GCT CTA GTT GCA GAG TTT CTT 4764  
asp phe ser glu ala ala met cys tyr val his val ala leu val ala glu phe leu

CAT CGA AAA AAA TTA TTT CCT AAC GGA TGT TCA GCG TTC AAG AAA ATT ACT CCC AAT ATA 4824  
his arg lys lys leu phe pro asn gly cys ser ala phe lys lys ile thr pro asn ile

GAT GAA GAA GGA GCA ATG AAA GAA GAT GCT GGG ATG ATG GAT GTC CAT TAT AGT GAA GAG 4884  
 asp glu glu gly ala met lys glu asp ala gly met met asp val his tyr ser glu glu  
 GTC TTG CTG GAG TTG CTA GAA CAA TGT GTG GAT GGC TTA TGG AAG GCA GAA CGT TAT GAA 4944  
 val leu leu glu leu leu glu gln cys val asp gly leu trp lys ala glu arg tyr glu  
 ATA ATT TCT GAG ATT TCC AAG TTG ATC GTT CCA ATT TAT GAG AAA CGT CGT GAG TTT GAG 5004  
 ile ile ser glu ile ser lys leu ile val pro ile tyr glu lys arg arg glu phe glu  
 AAA CTT ACT CAA GTT TAT AGA ACT CTT CAT GGA GCT TAC ACA AAA ATT CTG GAA GTT ATG 5064  
 lys leu thr gln val tyr arg thr leu his gly ala tyr thr lys ile leu glu val met  
 CAT ACA AAA AAG AGA CTT TTA GGC ACT TTC TTC AGA GTT GCC TTT TAT GGC CAA TCT TTT 5124  
 his thr lys lys arg leu leu gly thr phe phe arg val ala phe tyr gly gln ser phe  
 TTT GAA GAA GAA GAT GGA AAG GAG TAC ATC TAT AAA GAA CCA AAG CTC ACT GGC CTC TCA 5184  
 phe glu glu glu asp gly lys glu tyr ile tyr lys glu pro lys leu thr gly leu ser  
 GAA ATT TCC TTG AGA CTT GTT AAA CTT TAT GGT GAA AAG TTT GGT ACG GAG AAT GTC AAA 5244  
 glu ile ser leu arg leu val lys leu tyr gly glu lys phe gly thr glu asn val lys  
 ATA ATT CAG GAT TCA GAC AAG GTA AAT GCC AAA GAG CTT GAT CCA AAA TAT GCT CAT ATA 5304  
 ile ile gln asp ser asp lys val asn ala lys glu leu asp pro lys tyr ala his ile  
 CAA GTT ACT TAT GTG AAG CCT TAC TTT GAT GAC AAA GAA CTC ACA GAA AGG AAG ACC GAG 5364  
 gln val thr tyr val lys pro tyr phe asp asp lys glu leu thr glu arg lys thr glu  
 TTT GAA AGA AAT CAT AAT ATC AGC AGA TTT GTT TTT GAG GCC CCT TAC ACT TTA TCA GGC 5424  
 phe glu arg asn his asn ile ser arg phe val phe glu ala pro tyr thr leu ser gly  
 AAA AAA CAG GGC TGT ATA GAA GAA CAG TGC AAA CGC CGT ACA ATC TTG ACA ACT TCA AAC 5484  
 lys lys gln gly cys ile glu glu gln cys lys arg arg thr ile leu thr thr ser asn  
 TCG TTT CCT TAC GTG AAG AAG AGG ATT CCT ATT AAC TGT GAA CAG CAG ATT AAT TTA AAA 5544  
 ser phe pro tyr val lys lys arg ile pro ile asn cys glu gln gln ile asn leu lys  
 CCA ATT GAT GGT GCC ACT GAT GAA ATA AAA GAT AAA ACT GCA GAG CTG CAA AAG CTT TGC 5604  
 pro ile asp gly ala thr asp glu ile lys asp lys thr ala glu leu gln lys leu cys  
 TCC TCT ACT GAC GTG GAC ATG ATT CAG CTC CAA CTT AAA TTG CAG GGC TGG GTT TCT GTG 5664  
 ser ser thr asp val asp met ile gln leu gln leu lys leu gln gly trp val ser val  
 CAG GTC AAT GCT GGT CCA TTA GCA TAT GCA AGA GCT TTC TTA AAT GAC AGC CAA GCT AGC 5724  
 gln val asn ala gly pro leu ala tyr ala arg ala phe leu asn asp ser gln ala ser  
 AAG TAT CCA CCT AAG AAA GTG AGT GAG TTG AAA GAC ATG TTT AGG AAA TTT ATA CAA GCA 5784  
 lys tyr pro pro lys lys val ser arg glu leu lys asp met phe arg lys phe ile gln ala  
 TGC AGC ATT GCA CTT GAA CTA AAT GAG CGG CTA ATT AAA GAA GAT CAA GTT GAG TAC CAT 5844  
 cys ser ile ala leu glu leu asn glu arg leu ile lys glu asp gln val glu tyr his  
 GAA GGG CTA AAG TCA AAT TTC AGA GAC ATG GTA AAA GAA TTA TCT GAC ATT ATC CAT GAG 5904  
 glu gly leu lys ser asn phe arg asp met val lys glu leu ser asp ile ile his glu  
 CAG ATA TTA CAA GAA GAC ACA ATG CAT TCT CCC TGG ATG AGC AAC ACA TTA CAT GTA TTT 5964  
 gln ile leu gln glu asp thr met his ser pro trp met ser asn thr leu his val phe

TGT GCA ATT AGT GGT ACA TCA AGT GAC CGA GGT TAT GGT TCC CCA AGA TAC GCT GAA GTG 6024  
cys ala ile ser gly thr ser ser asp arg gly tyr gly ser pro arg tyr ala glu val

TGA GGA AAT GCA GAT GTA CGG TGA CAA TGA GAC TGA CCT TTC TCA GGA ATA TTT GGA GCT 6084  
OPA

GTG CAA ATG TTA AAA TTT AAA GAT TTG ATA TAC ATG GAG TGT TTC TTC TCG ACA CCA AAA 6144

TTT TCA TGT GTT CCA ACA GGG TGC TTA CAT ATT TGT AAA TAA GCA ACT TGA AAG TGC CTG 6204

GAA AAT TGC ACC ACT GTG CTT GGT TTG TAC TTT TTT AGG TAA ATC TAT ATG CTG AAA AGT 6264

AGA GCT CAA AAA CAG TAG TTC AAT TTG CTT AAT TAT TGC TTA AAA TAA TGG TAC TAT GTA 6324

AAA TTG TAT AAT GGA ATA CAA TAA AAG GTA AAA ATT

6360